FIG.1

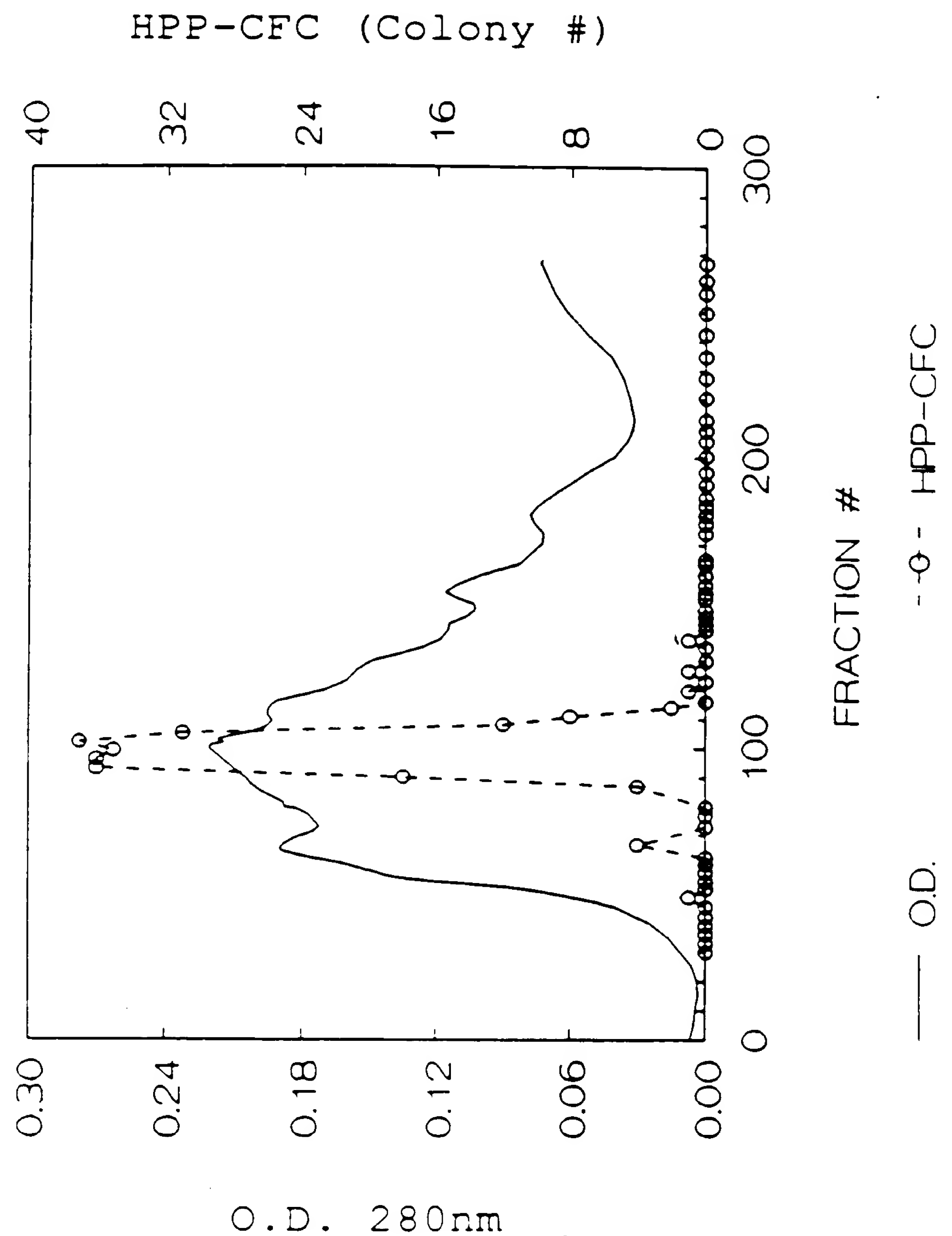

HPP-CFC (Colony #)
40
32
24
16
8
0
0.30
0.24
0.18
0.12
0.06
0.00
0
100
200
300
FRACTION #
O.D.
HPP-CFC
O.D. 280nm

FIG.2

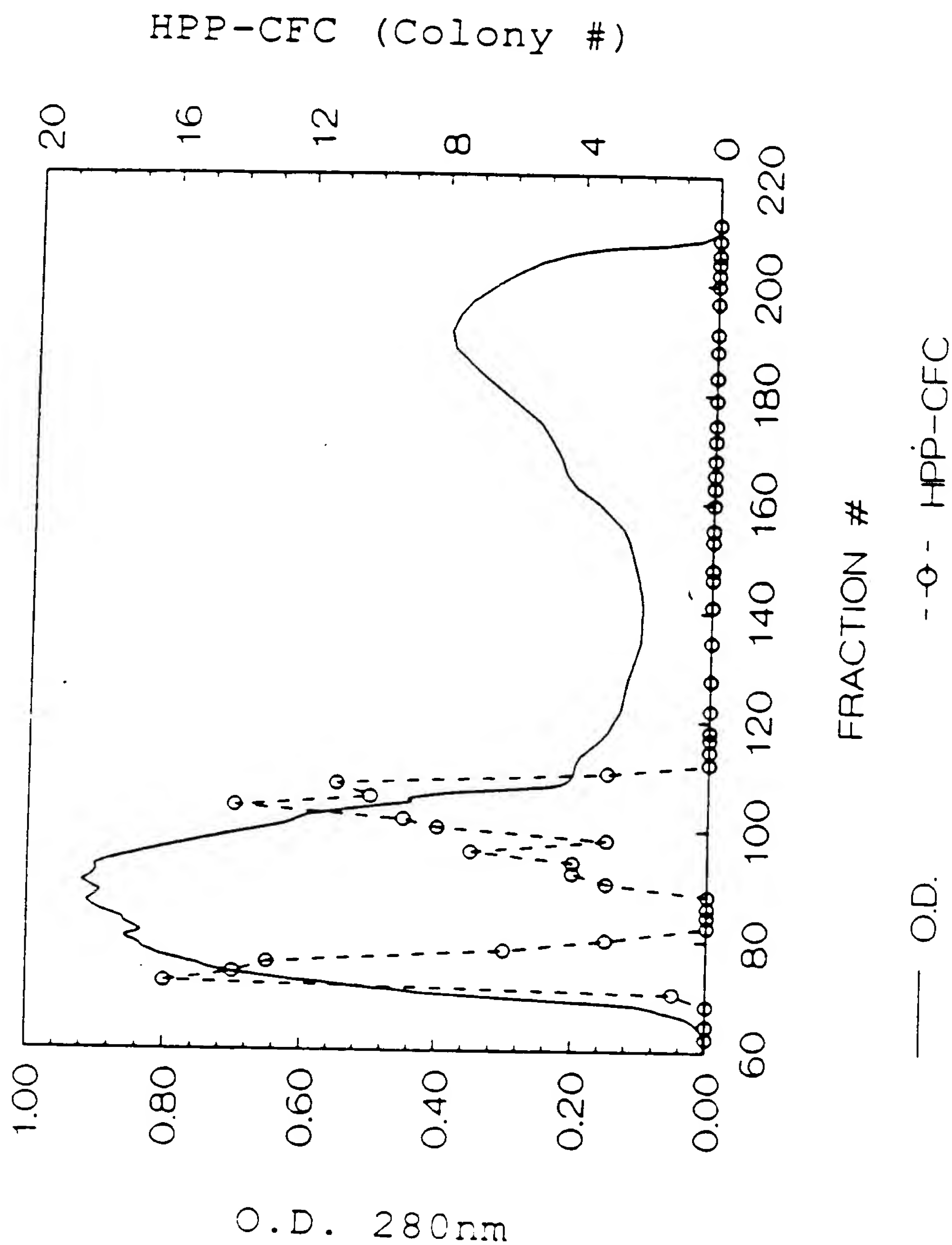
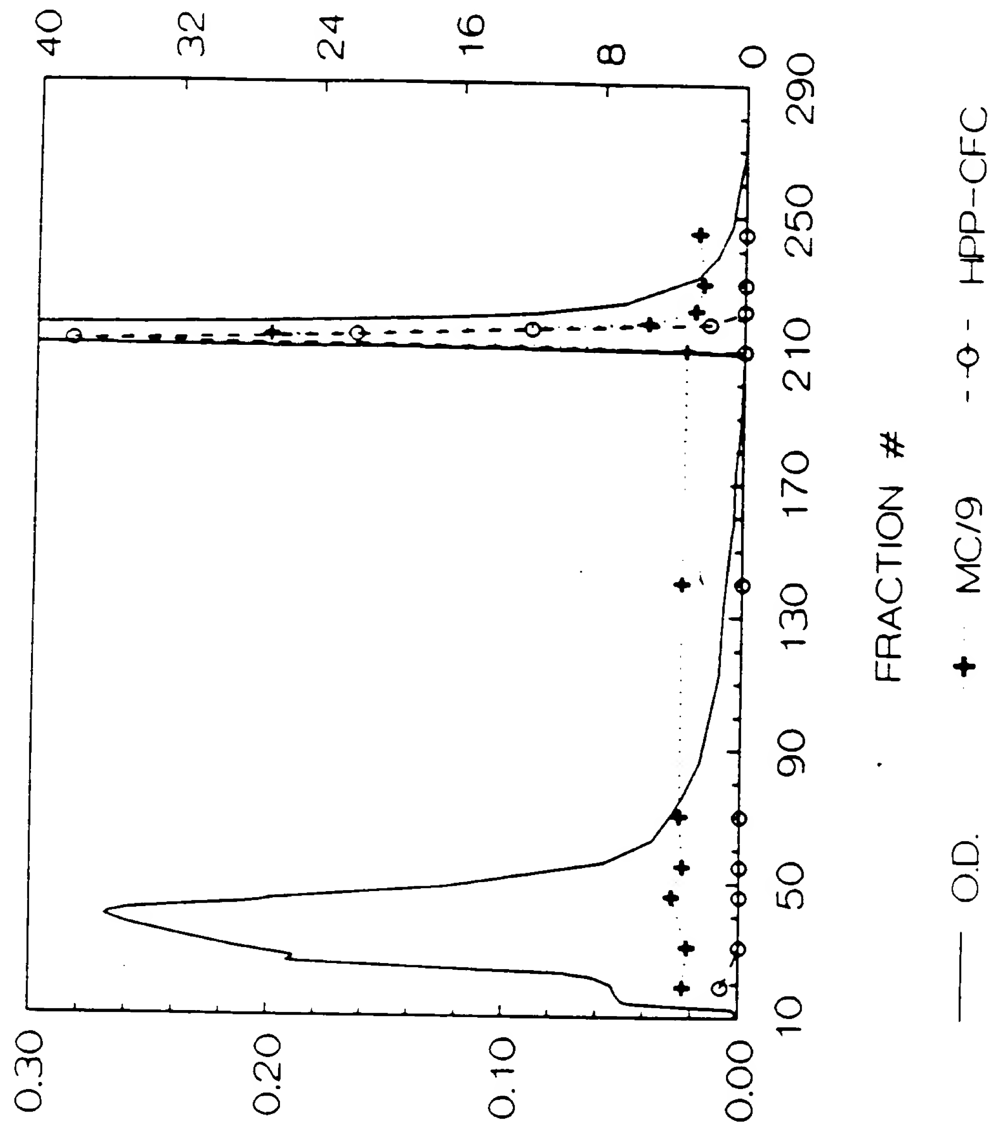

HPP-CFC (Colony #)
20
16
12
8
4
0
1.00
0.80
0.60
0.40
0.20
0.00
60
80
100
120
140
160
180
200
220
FRACTION #
O.D. 280nm
O.D.
HPP-CFC

FIG.3

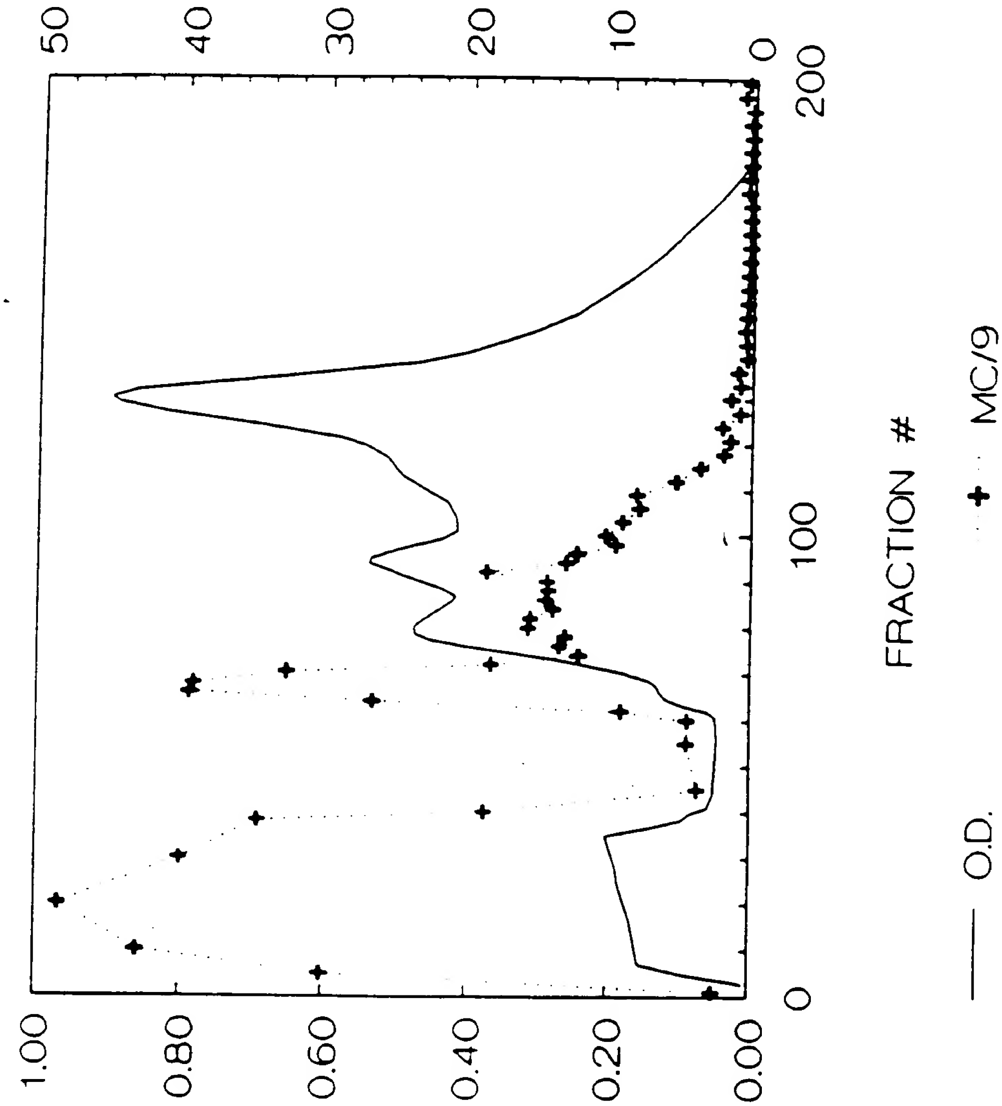
MC/9 CPM (X 10^{-3}) or HPP-CFC (col. #)



O.D. 280nm

FIG. 4

MC/9 CPM (x 10^{-3})



O.D. 280nm (x 10^{1})

FIG.5

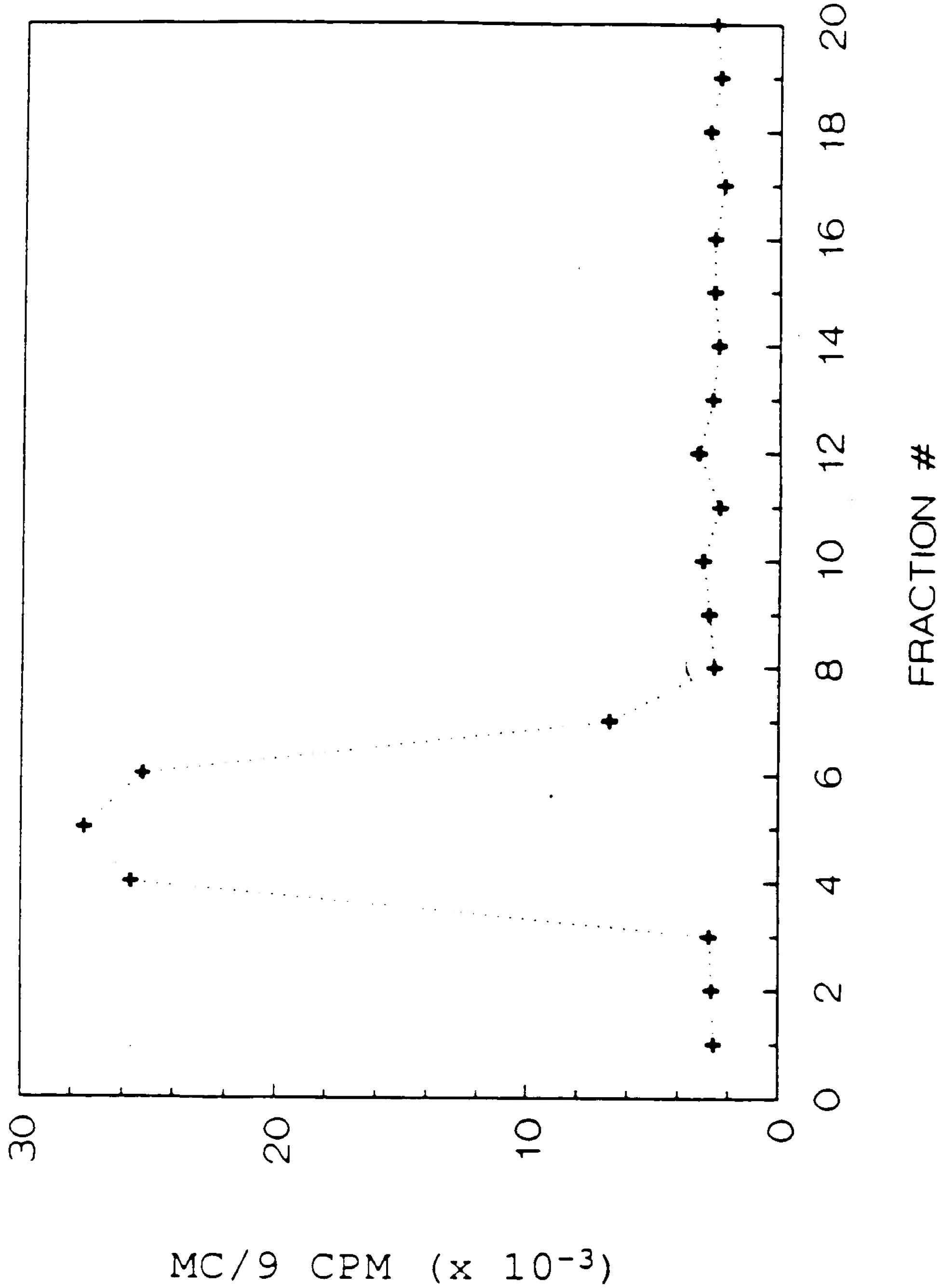


FIG. 6

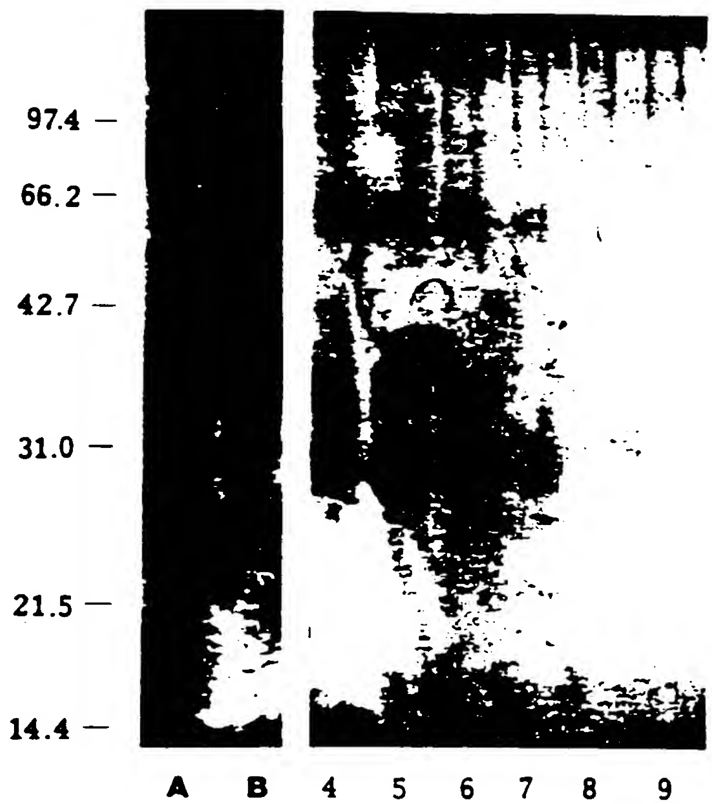


FIG.7

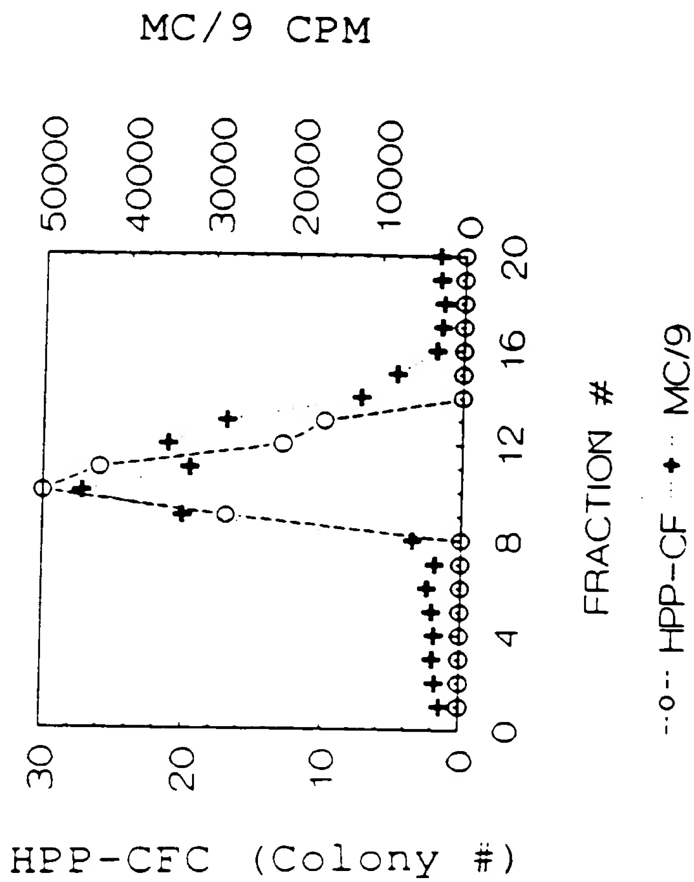

MC/9 CPM
50000
40000
30000
20000
10000
0
30
20
10
0
0
4
8
12
16
20
FRACTION #
--o-- HPP-CF ··+·· MC/9
HPP-CFC (Colony #)

FIG. 8

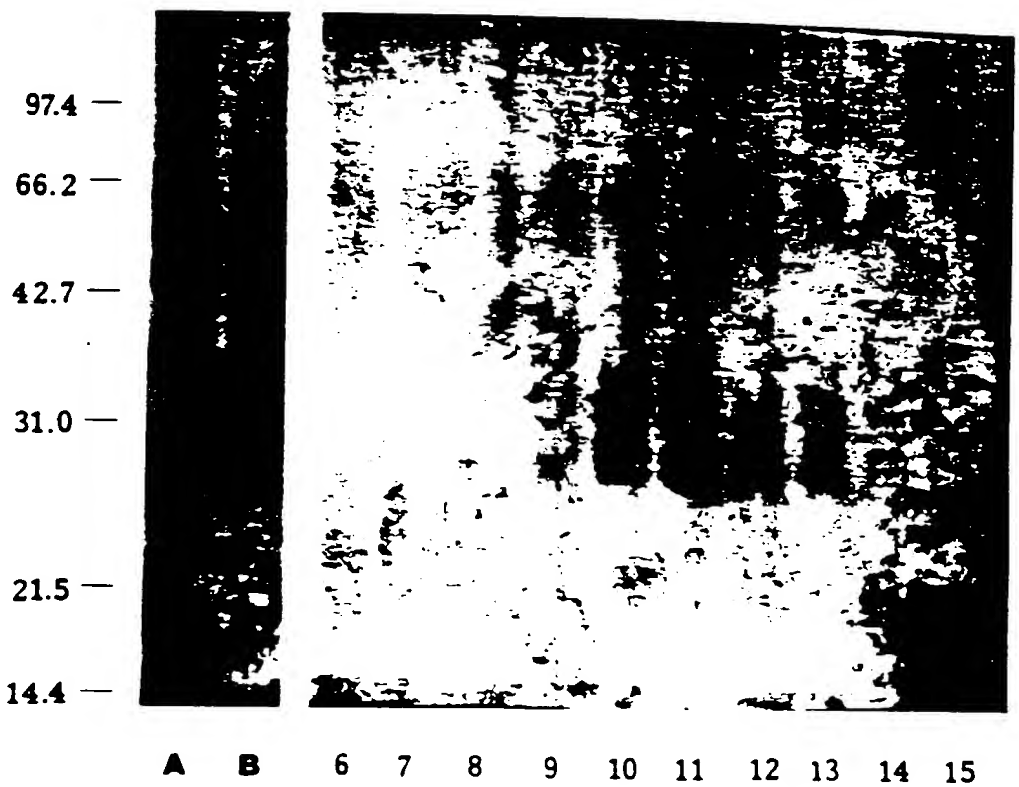


FIG.9

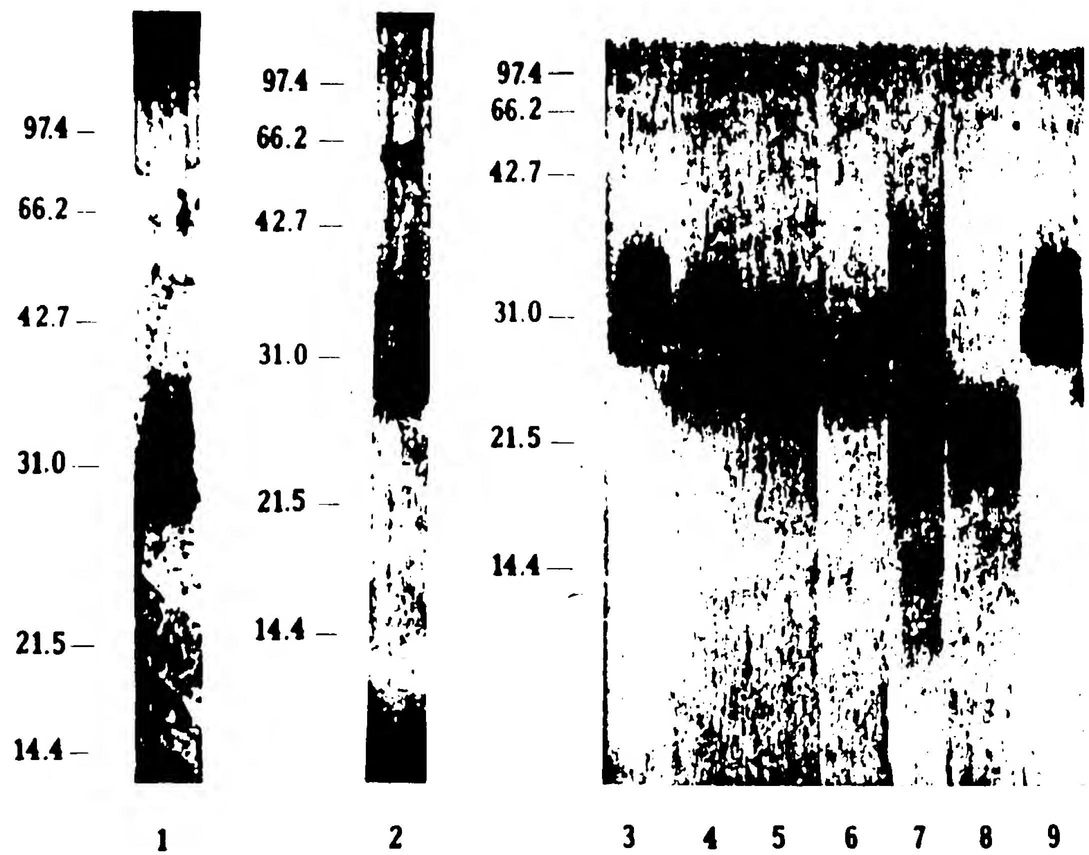


FIG.10

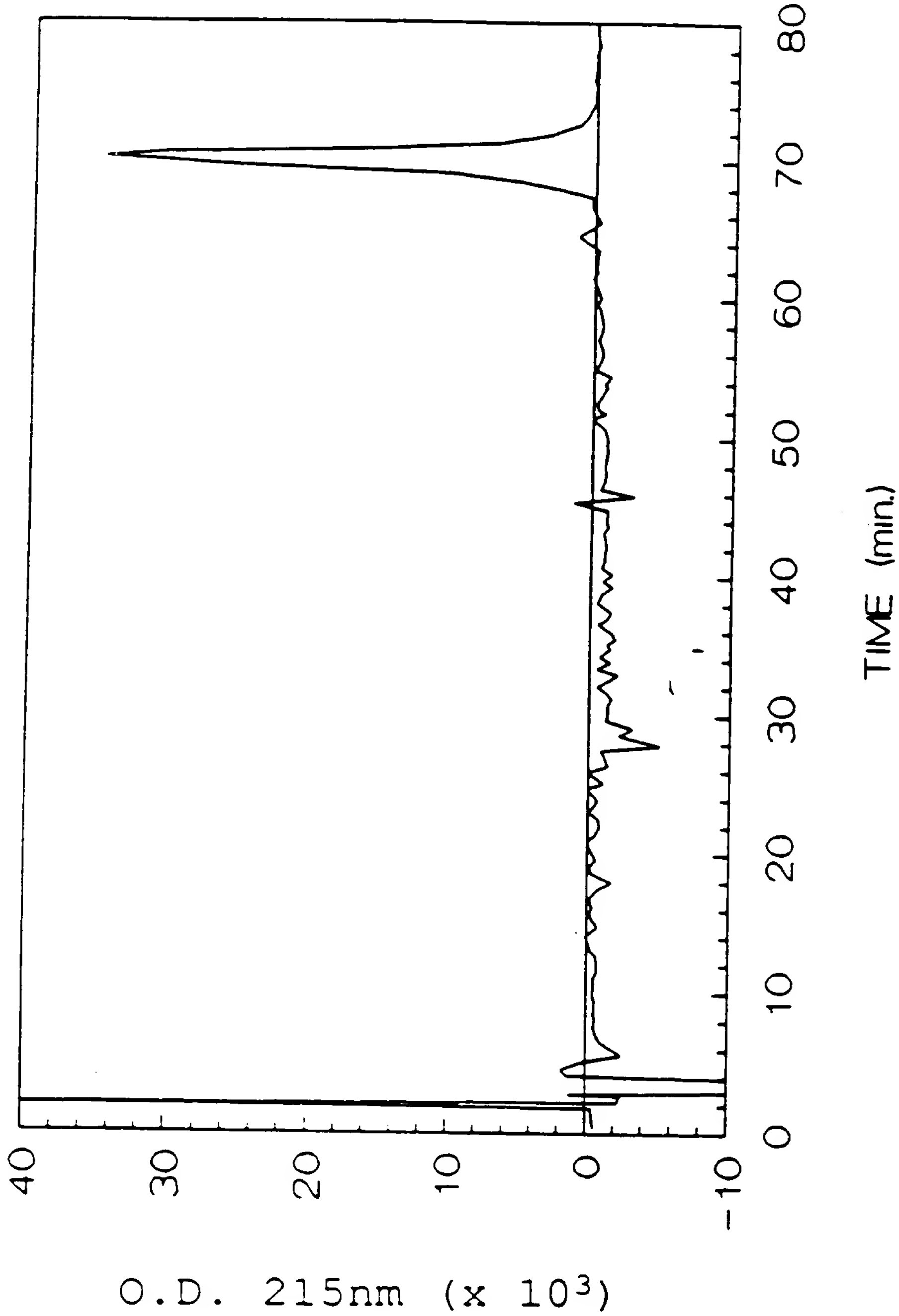


FIG.11

```
1                   10                  20
pE E I C R N P V T D N V K D I T K L V A N L P N D
  |--------------------------------------------- Sequencing after
                                               |-------- T-5a -------
            30                   40                   50
Y M I T L N Y V A G M D V L P S H C W L R D M V T
<Glu Aminopeptidase Treatment --------------->
                                                   |-----------------
------------------------------------- T-5a -----------------|
   |--------- CB-6a --------||------- CB-8; CB-10 ---------|
                    60                   70
H L S V S L T T L L D K F S N I S E G L S N Y S I
------ Sequencing after Trp Cleavage ---------------
            80                   90                 100
I D K L G K I V D D L V A C M E E N A P K N V K E
------------------------->
           ------------------ T-3 ------------------|       --
                                                              |--
                                          |-CB-14;CB-15;CB-16 -
                                              |-------- S-1---------|
                  110                   120
S L K K P E T R N F T P E E F F S I F N R S I D A
--- T-1 ----------------- T-4(N109 nonglyco) -----||-----------
----- T-7(N120 glyco);T-8(N109 nonglyco)-----
------------------------- CB-14; CB-15; CB-16 ------------------
|----------------- S-5 or S-6 (N109 nonglyco)-----------------
          130                   140                  150
F K D F M V A S D T S D C V L S S T L G P E K D S
----------------------------- T-5b ---------------------------------------
--------------------------------------------- CB-6B -------------------------
------ S-5 or S-6----------                                                -
                  160
R V S V T K P F M L P P V A(A)
--||---- T-2 ---                <-- <-- (Carboxypeptidase)
------ CB-6B ----------
----------------- S-2 ----------------------|
```

FIG.12A

```
OLIGO    SEQUENCE                        LOCATION

219-21   ACATTCTTIGGIGCATTCTCCTCCAT      393-368
           G  T        G  T  T

219-22   AAAAACTCCTCIGGIGTAAAATT         447-425
           G  T  T        G  G

219-25   GTTTCNGGTTTTTT                  420-407
           C     C  C

219-26   ATGGAAGAAAACGCCCCCAAAAACGT      368-393
              G  G  T        G  T

222-11   CCNAATGATTATATGATAAC            167-186
              C  C  C     C
                        T

222-12   GGNGGNAACATAAANGGCTT            566-585
                G   G     T

223-6    ACCATAAAATCTTTAAAICGATC         492-470
             G  G  C  G     G

224-24   GTATTTTCAATAGATCCATTGA          450-471

224-25   CCAACTATGTCGCC                  190-202

224-27   GTAGTCAAGCTGACTGATAAG           273-253
```

FIG.12A CONT.'

224-28	TAACCAACAATGACTAGGCAA	235-215	
225-31	TTCCAGAGTCAGTGTC	547-562	
227-29	GCGAAGCTTGCCTTTCCTTATGAAGAAGA	16-35	*
227-30	GCGCCGCGGTTACGGTGGTAACATGAAGGGCTTTGTGA	586-561	*
228-30	GATAAATGCAAGTGATAATCC	45-65	
230-25	GCGGTCGACCCGCGGAACTTTAAGTCCATGCAACAC	705-685	*
237-19	CACCCGCGGTTATGCAACAGGGGGTAACATAAATGG	569-592	*
237-20	CACCCGCGGTTAGGCTGCAACAGGGGGTAACATAAA	572-595	*

FIG.12B

OLIGO	SEQUENCE	LOCATION
231-27	CTTAATGTTGAAGAAACC	703-686
233-13	GATGGTAGTACAATTGTCAGAC	410-431
233-14	GTCTGACAATTGTACTACCATC	431-410
235-29	CAATTTAGTGACGTCTTTTACA	302-323
235-30	TTAGATGAGTTTTCTTTCACGCAC	556-533
235-31	AAATCATTCAAGAGCCCAGAACCC	566-589
236-31	AACATCCATCCCGGGGAC	366-383
238-31	CTGGCAATATTTTAAGTCTCAAGAAGACC	
241-6	GCGCCGCGGCTCCTATAGGTGCTAATTGG	
254-9	CCTCACCACTGTTTGTGCTGGATCGCA	153-179
262-13	GGTGTCTAGACTTGTGTCTTCTTCATAAGGA	209-190 *

FIG. 12C

```
OLIGO     SEQUENCE

201-7     CCCCCCCCGG
                 T
                 A

220-3     TTTTTTTTTTTTTTTTTTGG

220-7     TTTTTTTTTTTTTTTTTTAG

220-11    TTTTTTTTTTTTTTTTTTCG

221-11    TTCGGCCGATCAGGCCCCCCCCCC

221-12    TTCGGCCGGATAGGCCTTTTTTTTTTTTTT

228-28    GGCCGGATAGGCCTCACNNNNNNT

228-29    GGCCGGATAGGCCTCAC
```

FIG.13A

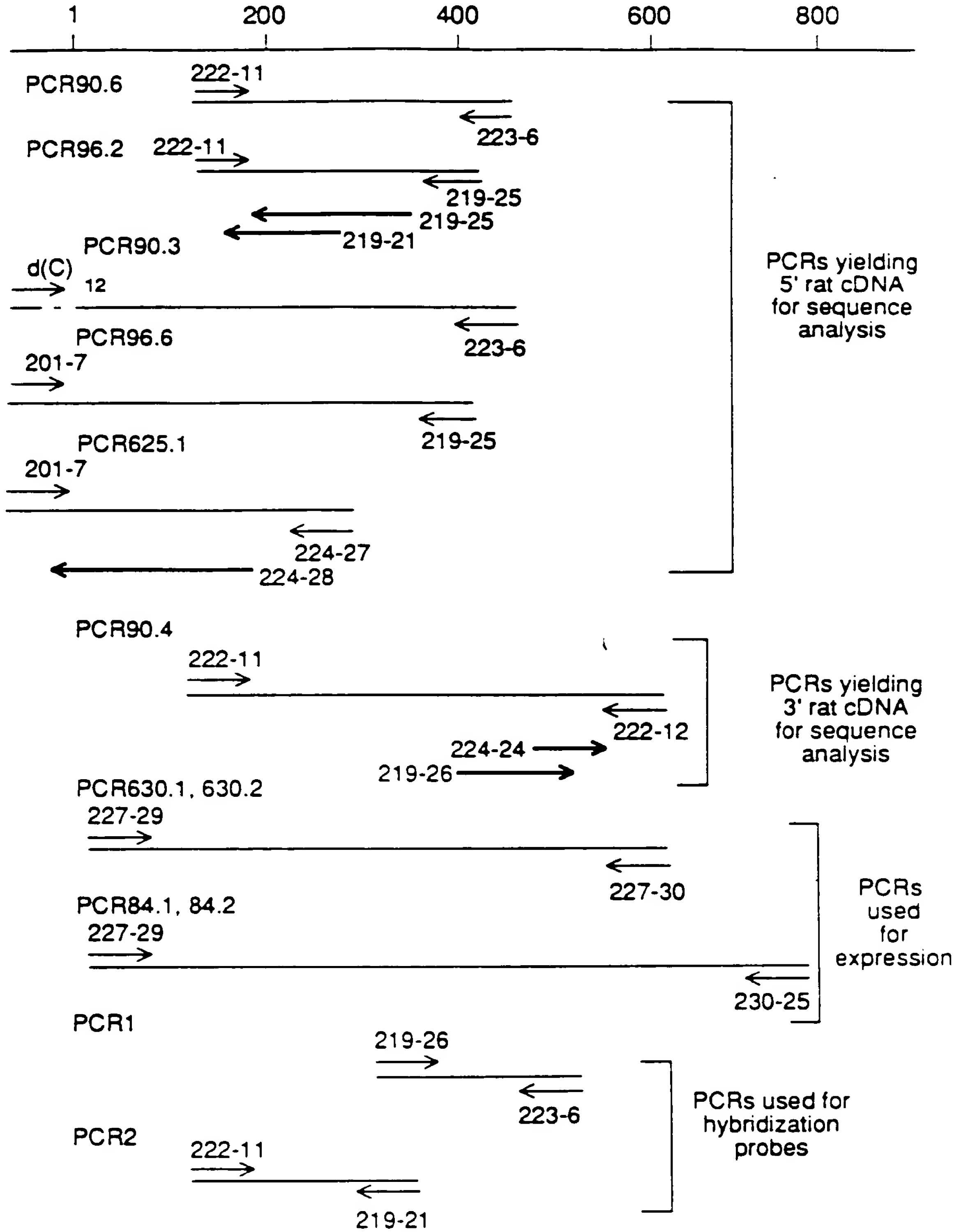

1
200
400
600
800
PCR90.6
222-11
223-6
PCR96.2
222-11
219-25
219-25
219-21
PCR90.3
d(C)
12
223-6
PCR96.6
201-7
219-25
PCR625.1
201-7
224-27
224-28
PCRs yielding 5' rat cDNA for sequence analysis
PCR90.4
222-11
222-12
224-24
219-26
PCRs yielding 3' rat cDNA for sequence analysis
PCR630.1, 630.2
227-29
227-30
PCR84.1, 84.2
227-29
230-25
PCRs used for expression
PCR1
219-26
223-6
PCR2
222-11
219-21
PCRs used for hybridization probes

FIG.13B

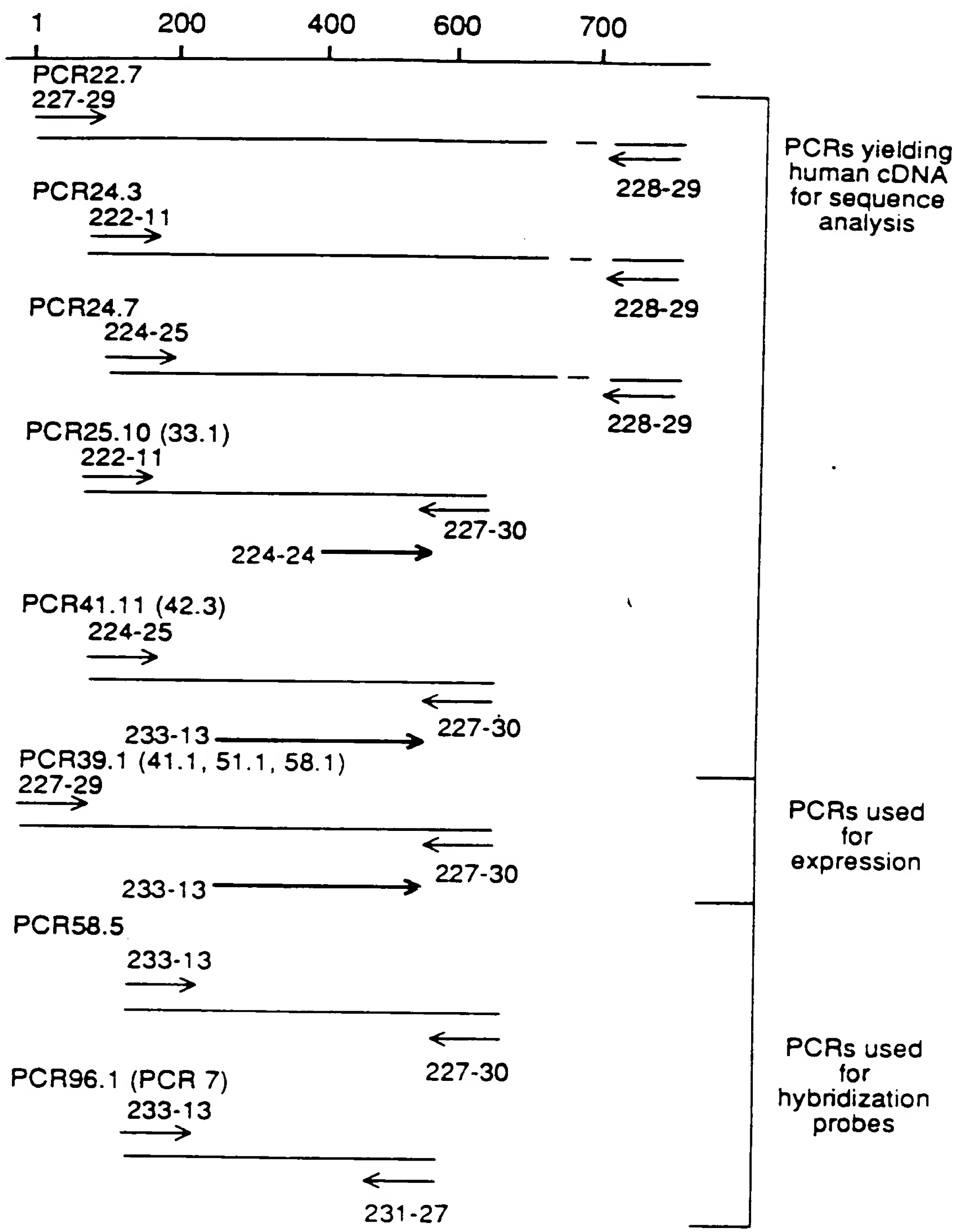

1
200
400
600
700
PCR22.7
227-29
228-29
PCR24.3
222-11
228-29
PCR24.7
224-25
228-29
PCR25.10 (33.1)
222-11
227-30
224-24
PCR41.11 (42.3)
224-25
227-30
233-13
PCR39.1 (41.1, 51.1, 58.1)
227-29
227-30
233-13
PCR58.5
233-13
227-30
PCR96.1 (PCR 7)
233-13
231-27
PCRs yielding human cDNA for sequence analysis
PCRs used for expression
PCRs used for hybridization probes

FIG.14A

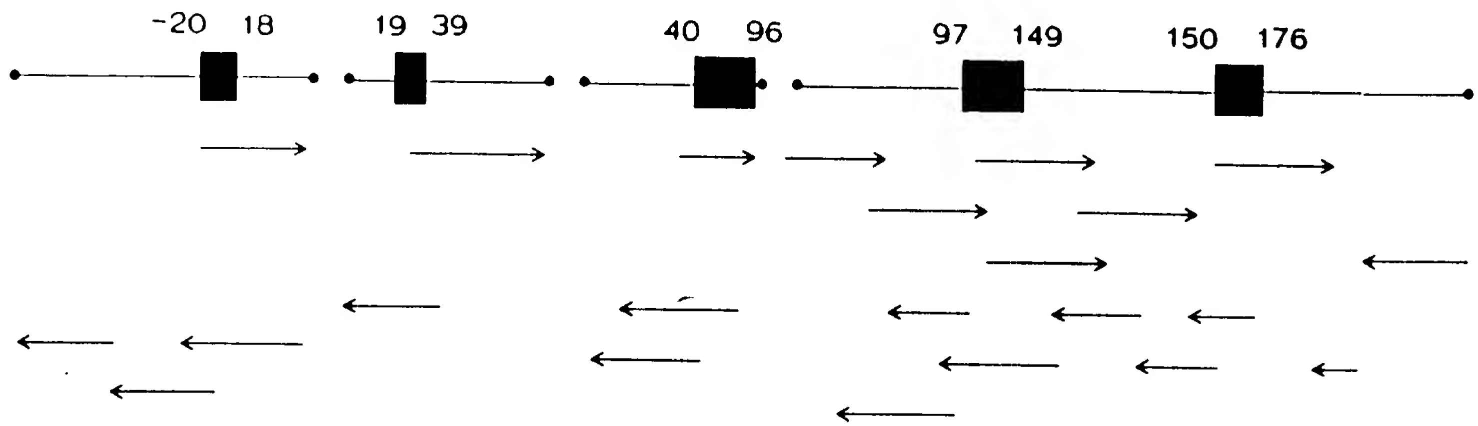


FIG.14B

```
AAAGTATCTTTCTATTGGCGAAGGACATGTTTTCCcATAAGTGGT    45
AAACAnACTGTCTGCACATAATAATTATCTTGCTGCCGTAAAGAT    90
TAGGTTAAATTCTGcCTTCGATCTAAAAACACACCCTTCTGTCAA   135
TCCGAGGAGCAGTGTGCTAGTCTAGAGGTCTAAATGAAGGCTCCT   180
TTCACGGTTGTATTTCTGCTCCCCAAATTGTCCACATTTAAAAGG   225
AGAGTGCTTCTTTTCAGCCTTAGGCTCTGAATTTCATGCATTCCT   270
CCATTTTCCGAGGTCCCccCcAAGTGATAATTCTGTTACACGTTG   315
CTACAAGTTCATCCCTAATTGCCGTCAAGAAACTGACTGTAGAAG   360
GCTTACCACAGACGTTGTAACCGACAGTAAAGCCATTGAAAGAGT   405
AATTCAAACAGGATGGAAGCCAGGAGTATTTTGTGGCTGTTGCTC   450
TTTTTCTTTTCAGTTTGGTGAGAGCAGCTTGAATGCTTAACATTT   495
AAGCCATCAGCTTAAAACAAAACAAAACAAAACAAAAAAAAACCC   540
CGCTCTGGCATATTTGCACTTAACACATACGGTATAAGGTGTTAC   585
TGGTTTGCATAGTTCTGGATTTTTTTTTTTAAAAACTGATGGAC    630

                                    -20
                                    ThrTrpIleIleThrC
ACCAAGAAATGTTTCTGTTCTTTGTTTAGACTTGGATTATCACTT    675

                -10
ysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrG
GCATTTATCTTCAACTGCTCCTATTTAATCCTCTCGTCAAAACTC    720

 1                          10
lnGluIleCysArgAsnProValThrAspAsnValLysAspIleT
AGGAGATCTGCAGGAATCCTGTGACTGATAATGTAAAAGACATTA    765

     18
hrLysLeu
```

FIG.14B CONT.'

```
CAAAACTGGTAAGTAAAGAATGATTTTGGCATCTATAAGTCTTCC   810

CTGTGCTTGCTGACCACATAGGTTCAGGGCACTCCCGACAGGAGT   855

TCCCAGCTTTCTAAGATAAGGAATCACTGTACGAGTCTGAAGTGC   900

TTCTTCTGGGCAAATGGGAGATGCTTAGGTCATGGAGGGTTTATC   945

TGTATAACTGGCCCTTTGCACACCAACAAAGTGACTGACTGGCTT   990

TTGCCTGTTACCTACTG                              1007

     Intervening sequence of unknown length

TCTCCAGTCCTGGGCATGGTATATACTTAGGCACCCAAGATTGGA   45

TTTACAACTCAAGCATTATATATTGGACAACnACGGGGTATGAGA   90

TATTAATGATATGTCAGGTTGGATGGATGAGTTTTCTCAAGAAAT   135

                                           19
                                          Val
TCTCTTGTATTTACTCACGTTTTCATTTCTTGGTCTCTGTAGGTG   180

                                 30
AlaAsnLeuProAsnAspTyrMetIleThrLeuAsnTyrValAla
GCGAATCTTCCAAATGACTATATGATAACCCTCAACTATGTCGCC   225

            39
GlyMetAspValLeu
GGGATGGATGTTTTGGTATGTAGTCCACACACTTCTGAGTTGCCT   270

TTTAGTAGCTAATGGGTGACCTGTGCTTATTCACATTGAAGACAT   315

TATTTGCTCTTTGTCGTTTTTAGATGTTGACCTATAATTTTTCCT   360

TCAAGCTGCTGCTAAGATTATCAGTGAGCATTTCAGTATGTGTTT   405

TAAGCCTACTCATTAAAAGGAAATGGCTCATCTTAGACGTAGCAA   450
```

FIG.14B CONT.'

CCGATGTTAATTTTTCCCCAGGCATCTCTCAGAGGGACTTGAATG 495

TTAAAATCATGTTAAATTTCCTCCTTGGCTATGTTATTTCTCATG 540

GCTATGTTATTCCTATTCGTATTTCATTTAAAGGGACGGAATATT 585

TATTGTATTTCTGAACTTTTTCAGGCATGCATCCGGGTCTTTGAA 630

TAAAA 635

Intervening sequence of unknown length

CACTAAGACTCCTTCTAGTAATGTTTGTAATCCTGTCTGTATCGA 45

ATGTCTTTGAAAACGCAGTGACTAAGCCATAAATAATCTTCCACA 90

GAACGTCCAGTGGTTCATGAACTTTGTATGTGGGGTGGGGCAAG 135

AATTGTCTCACTATTGGTCAAGGAAGAGAAGGTAAGGTATGCAAG 180

GGTGGTTTAATCTTCTTCCGTGGAAGGACAAAATCATCTATCATT 225

TCCTCTGATCTCTATGCATTTGTTTGTTTTGAACTGAATCTGACT 270

TGAGCAAGAGTTGGCGTCCTGTGTTCTGAGGAAACTCTTTGTCCT 315

GCAGTCAGTGACTAAAAGTGCTGAGAGATCTGAAGAGCACTCTGA 360

ATCTGCCATATTTTTAATAGATGCTTTGTCTTCTCTTTGAATTTC 405

40 50
ProSerHisCysTrpLeuArgAspMetValThrHisLeu
TTCCAGCCTAGTCATTGTTGGTTACGAGATATGGTAACACACTTA 450

60
SerValSerLeuThrThrLeuLeuAspLysPheSerAsnIleSer
TCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTTCT 495

70 80
GluGlyLeuSerAsnTyrSerIleIleAspLysLeuGlyLysIle

FIG. 14B CONT.'

GAAGGCTTGAGTAATTATTCCATCATAGACAAACTTGGGAAAATA 540

```
                        90                  96
ValAspAspLeuValAlaCysMetGluGluAsnAlaProLys
GTGGATGACCTCGTGGCATGTATGGAAGAAAATGCACCTAAGGTA 585
```

ACTTGGTATTCATCAGAATTATTTTTCTTATACT 619

Intervening sequence of unknown length

GAGCTCATGATGAGCAATTCACAACCACTTGTAATTCCAGCTCCA 45

GAGGACATTATCCCCTCTTTGGATGCCATAGGAATCTGCTCTCAA 90

ATATGTAGATACCACCTCTGCCACCTCAGCACATACATACACATA 135

ATTAAAAAATAGAAACATTAAAGGAGTTCCAATCAATCCTTATTC 180

TTTTCTGTATTCAGTATGCCCAGATGTAAATTCTAGGAATATGTT 225

TTAAAGGCTAATTCTTATTTTGTAATAAGCAGCTTTAAAATTCTT 270

AATTGTTTTTTCGGGTCACTTTATTGTCCTATTGCCACGACATTG 315

TCCTGTCCCATTGTCTGTTATTCCTTCTGTTTTGTTTATTGTTCC 360

CTAGTTACTTTGATCATGAGATTGACCTGTTACCCGTTGTTATTC 405

TCTGTAGCCATTTTGAGTTGTGTCTATTAGAACAGCTGTTAAATT 450

ACTTGAATCATTGAGGACATAGTCAATAATCTATTATGCTGATCC 495

AGTCAAGTCTATGAGTTATTTGAAAACTAGAATCTTTGTTAATTA 540

```
                                         97
                                      AsnValLys
TTTGTTTGCTTGTTTGTTTGTTTATTATTTGTCTAGAATGTAAAA 585

100                    110
GluSerLeuLysLysProGluThrArgAsnPheThrProGluGlu
```

FIG.14B CONT.'

GAATCACTGAAGAAGCCAGAAACTAGAAACTTTACTCCTGAAGAA 630

120
PhePheSerIlePheAsnArgSerIleAspAlaPheLysAspPhe
TTCTTTAGTATTTTCAATAGATCCATTGATGCCTTCAAGGACTTC 675

130 140
MetValAlaSerAspThrSerAspCysValLeuSerSerThrLeu
ATGGTGGCATCTGACACTAGTGATTGTGTGCTCTCTTCAACATTA 720

148
GlyProGluLysA
GGTCCTGAGAAAGGTAAGGCTTTTAAGCATTTCTTGTTTAAATGT 765

ACATAGAAAGCCTGAACTTCTGTAAGCCTCTACTGCTGAATCAAC 810

TAAATGTGTTGCTGTAGAAAGAACGTGTGGGTTTTTCTGATAAAA 855

ACAAAAAGCAAATATCAATGACTACCAATGATTATTATCTAGCTT 900

GAGAGATATGCCCTAAGACAGCGATTCTCGATATTTCTAAATTAA 945

AGAATTGTGTGATGGTGGCTCACATATTTTCTAACTGTGATATTT 990

GCCAGGAGAGTAGAATAATGTTATTCTTCATCCCCAGAATTCCTA 1035

AGATTTCACGTCTCATGTCTTTTCCATAAGGTTCAAACTCTGAGA 1080

CTTGAGTTCTGAGCCTCAGCAGGTCATTCTGAATCCCCACTCTCC 1125

CCGAGCTGGGTCCCTATGGGGGAACTAACTTCATTGCTTTCTTTT 1170

AAAACATGACGAGTTACCAACAGCTCCTCGCTATTATAAACATGT 1215

TCCTAAGCATGTCTGTGCATGCaATAAGCCTTCACTCTACAAGAC 1260

AGTTATGGTGTATCGCTTGACAAAACTGAGCAGCCAAGCTGAGTA 1305

TGAAATAATAATCTAGACTTGGGAGGCAGACCCAGCACCTACTGT 1350

GATATTGCACTTCGCCTTTGGGGGACTCTATGATTCAAAAGTTCA 1395

FIG.14B CONT.

```
                                                  150
                                                spSerArgV
CCATGTAACACTGACACATTATTGCTTTCTATTTAGATTCCAGAG     1440

                      160
alSerValThrLysProPheMetLeuProProValAlaAlaSerS
TCAGTGTCACAAAACCATTTATGTTACCCCCTGTtGCAGCCAGTT     1485

        170              176
erLeuArgAsnAspSerSerSerSerAsn_
CCCTTAGGAATGACAGCAGTAGCAGTAATAGTAAGTACACATATC     1530

TGATTTACTGCATGCATGGCTCCAAGTATCCTCTATAGGAGTGTT     1575

GCATGGACTTAAAGTTTATAAATCACTACTAATAATGCTGTTCTG     1620

TCACTGTTATTCCTTGTATGGGCTTCCTGACAATTAAATATCTGG     1665

TTTGTAGAATCGGATCTCCTTAGAGGTTAAGATGACCATGACAAA     1710

ATTAGGCCAATCAACTTTCTGCGAAGGTTATTTAAATAAGGCAC      1755

GAAATTAATTGAAGGAAAAAAAAATACAAGCAAGGCCTTATTTTG     1800

AATCATGGTAGGCTTAAAATAGACTTTGTGGAGAATGTCCCTGAT     1845

CAAAGTGGAGTTTTCAGATTTCAAGTGCATGTGCTAACTCTCCAC     1890

AATGTCAAGGCTATTTTCAGTTTTGTGTCTCCATATTTACTACTG     1935

CATGTTTGGAAATTTGCTGATGCTGTTAGATTACCTAAGAATGTA     1980

TGTTGAAGAAGAATGGACTTCTTTCCCTAAAATTTCTGTCCTCTT     2025

TGcCCAAGAACCCAcGTTCCTGGAAGACTATCTTATTTTCATGTC     2070

TGTGCAATGATCATTATAAAGATTATTGAATATACTGGGAATACT     2115

CTGGTTTCTGTTTTTACAGATTCATAATAGCTTATTCAGTCTTTA     2160

AAGAAAGTTCTCTGAAGTCCATGCTTTAGAATGTTTCTCTATCAA     2205
```

FIG. 14B CONT.'

AACTTGACCTGGACCTTAAATAAAGCTATATTTAGTCTTTTTATC 2250

CCTGAAAAATATATTTCACAGTGTAGACATTTGATATACATCTAA 2295

GGGAAGGATGCTGCCAGAATGCTCGGGCTGGCAGTCTACAAAGTC 2340

CACTGCTCTCAGGATGGACTTCTGAAAGCGGAAATTGTGAACTGC 2385

ATGCATATAACATATCAGATCCTCGAGC 2413

FIG.14C

```
                                   -25               -20
                                   M  K  K  T  Q  T  W  I  I  T  C  I
CTGGATCGCAGCGCTGCCTTTCCTTATGAAGAAGACACAAACTTGGATTATCACTTGCAT   60

       -10                                   1
 Y  L  Q  L  L  L  F  N  P  L  V  K  T  Q  E  I  C  R  N  P
TTATCTTCAACTGCTCCTATTTAATCCTCTCGTCAAAACTCAGGAGATCTGCAGGAATCC  120

       10                                20
 V  T  D  N  V  K  D  I  T  K  L  V  A  N  L  P  N  D  Y  M
TGTGACTGATAATGTAAAAGACATTACAAAACTGGTGGCGAATCTTCCAAATGACTATAT  180

       30                                40
 I  T  L  N  Y  V  A  G  M  D  V  L  P  S  H  C  W  L  R  D
GATAACCCTCAACTATGTCGCCGGGATGGATGTTTTGCCTAGTCATTGTTGGTTACGAGA  240

       50                                60
 M  V  T  H  L  S  V  S  L  T  T  L  L  D  K  F  S  N  I  S
TATGGTAACACACTTATCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTTC  300

       70                                80
 E  G  L  S  N  Y  S  I  I  D  K  L  G  K  I  V  D  D  L  V
TGAAGGCTTGAGTAATTATTCCATCATAGACAAACTTGGGAAAATAGTGGATGACCTCGT  360

       90                               100
 A  C  M  E  E  N  A  P  K  N  V  K  E  S  L  K  K  P  E  T
GGCATGTATGGAAGAAAATGCACCTAAGAATGTAAAAGAATCACTGAAGAAGCCAGAAAC  420

      110                               120
 R  N  F  T  P  E  E  F  F  S  I  F  N  R  S  I  D  A  F  K
TAGAAACTTTACTCCTGAAGAATTCTTTAGTATTTTCAATAGATCCATTGATGCCTTCAA  480
```

FIG.14C CONT.'

```
   130                                 140
 D  F  M  V  A  S  D  T  S  D  C  V  L  S  S  T  L  G  P  E
GGACTTCATGGTGGCATCTGACACTAGTGATTGTGTGCTCTCTTCAACATTAGGTCCTGA   540

   150                                 160
 K  D  S  R  V  S  V  T  K  P  F  M  L  P  P  V  A  A  S  S
GAAAGATTCCAGAGTCAGTGTCACAAAACCATTTATGTTACCCCCTGTTGCAGCCAGTTC   600

   170                                 180
 L  R  N  D  S  S  S  S  N  R  K  A  A  K  S  P  E  D  P  G
CCTTAGGAATGACAGCAGTAGCAGTAATAGGAAAGCCGCAAAGTCCCCTGAAGACCCAGG   660

   190                                 200
 L  Q  W  T  A  M  A  L  P  A  L  I  S  L  V  I  G  F  A  F
CCTACAATGGACAGCAATGGCACTGCCGGCTCTCATTTCGCTTGTAATTGGCTTTGCTTT   720

   210                                 220
 G  A  L  Y  W  K  K  K  Q  S  S  L  T  R  A  V  E  N  I  Q
TGGAGCCTTATACTGGAAGAAGAAACAGTCAAGTCTTACAAGGGCAGTTGAAAATATACA   780

   230                                 240
 I  N  E  E  D  N  E  I  S  M  L  Q  Q  K  E  R  E  F  Q  E
GATTAATGAAGAGGATAATGAGATAAGTATGTTGCAACAGAAAGAGAGAGAGTTTCAAGA   840

248
 V
GGTGTAATT                                                      849
```

FIG.15A

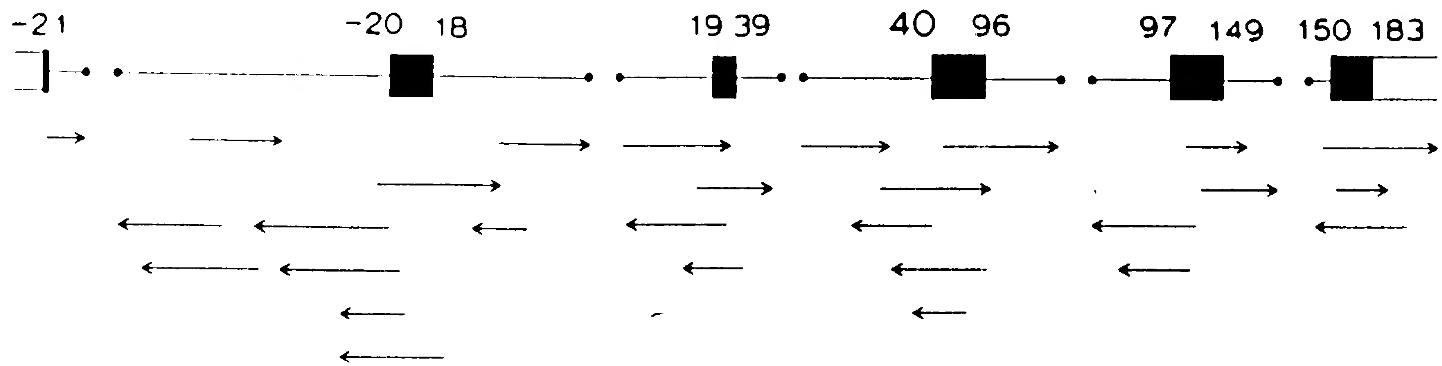


FIG.15B

-21
hrGln

CACAAGTGAGTAGGGCGCGCCCGGGAGCTCCCAGGCTCTCCAGGA 45

AAAATCGCGCCCGGTGCCCCGGGGaAGCCGGCGCTCCCTGGGACT 90

TGCAGCTGGGGCGTGCAGGGCTGTGCCTGCCGGGTG 126

Intervening sequence of unknown length

AGATACTACAAAGATAAATCAGTTGCACAAGTTCTTGAAACTCTA 45

CAGTGTAATAAGGAAAAATAAGTCATGCATAAAAGCAACTATAAT 90

ACATAATAGAAAATGTTATTTTCAAGCCGATGTGTAGGTTATGTG 135

TGTTCGAGAGAGAGAGAGAGAAGACAGATTACTTTCTGCTAGGGT 180

TCAAGAATGCCTTCCTGTTGGCTAAGGAAATATTTTCCTTAAGTG 225

GCTAAAAAGCTGTGTTTCAAAATATTCTTTTGATGTCTCACAAAT 270

TCAGTGGAATTCTCTTAGGTCTAAAAATATACATCTCTCTCACTT 315

TAACTTGGTGTGCTATTGTAGATTATTGGATTAAAGCACTGCTCA 360

GGGATTATGCTGCTTCTTGCCAAGCAGTCTACATTTAAAGTAGAA 405

ATAAGATGTTTCTTTTGGTGCCATAAGGTATACATTTTATGCATT 450

CTCTAGTTTTTAGAAGATACCCTAAGGGCTAAGTCTTTAACATGC 495

TGCTACAAGTTTATTCCTAATTGCCATTGGGAAATTGGCTGAAGA 540

AAGTTTTTAACAAAAGTTAACAATATTGTCATTGAGAGAATAATT 585

CAAAATGGATTTTAACTAAAAGCTTTTAAAAACTTTGGTGAGCAT 630

AGCTTGAATGCGTAATATTTAATTGCATTTAAGCCAATAACATAT 675

FIG.15B CONT.'

```
ATTAGACTGGTCTTTTTGTGCATCAAGGCATTAGATGTTAAAAGT    720

TTGAATGATTACAGATCTTAACTGATGATCACCAAGCAATTTTTC    765

                  -20                                 -10
                  ThrTrpIleLeuThrCysIleTyrLeuGlnLe
TGTTTTCATTTAGACTTGGATTCTCACTTGCATTTATCTTCAGCT    810

                                        1
uLeuLeuPheAsnProLeuValLysThrGluGlyIleCysArgAs
GCTCCTATTTAATCCTCTCGTCAAAACTGAAGGGATCTGCAGGAA    855

         10                                18
nArgValThrAsnAsnValLysAspValThrLysLeu
TCGTGTGACTAATAATGTAAAAGACGTCACTAAATTGGTAAGTAA    900

GGAATGCTTTACCGTGCTGTGTAAAAAAGAGCTGTGGCTCTTTTT    945

CCTGTGCTTGTTGATAAAAGATTTAGATTTTTCTTGCCCCAAAGT    990

AATGTTTTCCTAAAGTGGGGAAAGTAATCACTGGGTTACAATAAA    1035

GGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA    1080

TTTGTTGGTAAAACTGGCTAGTTGCACACCACTGCTGTGACTGCT    1125

TCTTTGCTGGTCTTCTCCCCATCCTTCATAGGCAGTGAAGGACCT    1170

TGGAGAGTTCGCTGTGTGCTGATGGGCTTGCCCCAGCTTGTTCCC    1215

CATAATCTCTCCAGTGGGTTTCCCAGCATGTTCTATTCCCCTTCA    1260

CATGTCTTCCTACTCTTCTTTAAAAAGCCTAACGAAAGGAAATCT    1305

GAAATGGCTATTCTCCCAATTCAATCAGCAGGAAGACCCTGTCAC    1350

ATGTCAGTGGGTGTTTGCTCCTTCAGGGAACATAGAGAGGTGATT    1395

CATTGCCCACATGTTGAAGGGACTCATCTCCCTGGTTTGTCACAT    1440

TGAACTCTTCCCTCAGCGAAAGCATTTGCATTGCTTCCC          1479
```

FIG.15B CONT.'

Intervening sequence of unknown length

```
GAATTCCAAGATCACAGGTGGAAGCTGAAATTCAGATCATGTTTC    45

CAAAACTCAGTAGGTTATACCTAGCCAGGCATAACTGAATTTGGA    90

GTCTAAAAGATCTGTATTATCACTTTTTATTTTGAAGGATGCCT     135

TTTGATTACAGAGGGAAATCAAGGATTAAAAATCAATATACATGT    180

AAATATTGAAATTCATTGGTAACTTTAAAAAGCACAACAGTTTTG    225

TGTGCTTTTCTCCAAAGCACTACAAATATGATTAATTGATGTATA    270

                                       19
                                     ValAlaA
AGAATTTTCTTATGGAATTTTTTTTTTGTCTCTGTAGGTGGCAA     315

                          30
snLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM
ATCTTCCAAAAGACTACATGATAACCCTCAAATATGTCCCCGGGA    360

          39
etAspValLeu
TGGATGTTTTGGTATGTAAACTACATTTCTGAGTTTCATTTTAGT    405

AGCTCATAGAAGAAATGGGATCATTCATATTGAGATAGTACACTA    450

GCTGCTATTTAGGAGCTTGCTTATTGTCAGGATTTGAAGAATTTA    495

TCTTTGGAATTTGACTTGCAGGCTTTTTTTCCCCCTCTT   535
```

Intervening sequence of unknown length

```
CCTGTTACAAGAGTCCCTCCTCCTATTAGAATAGTCCCTCCTCCT    45

CCTGTCACACTAGTCCCTTCTCTTCCTGTTACAATAACCCCTGTC    90
```

FIG.15B CONT.'

```
CTCCTATTACAACATTTTAAGTAATGTAATATTAATTTTAAAAAT   135

CTGGCCAGGCACGGTGGTTCATGCTTGTAATCCCAGCACATTGGG   180

AAGCTGAGACGGGTGGATCATTTGAGGTCAGGAAGTTTGAGACAG   225

CCTGGCCAACATGGTGAAACTTCCTCTCTACTAAAAATAAAAAAG   270

TAGCCAGGCATGGTGGCAGGCACTTGTAATCTGAGCTACTCGAGA   315

GGCTGAGGCAGGAGAATCACTTGAGTAACTAAAACGATAGCTTTG   360

AAGAGTACTCCGAGTTTTATGGCACTTACTTATTAAAATAGCTGT   405

                           40
                         ProSerHisCysTrpIleS
TTTGTCTCTTTTTTCATATCTTGCAGCCAAGTCATTGTTGGATAA   450

           50                                60
erGluMetValValGlnLeuSerAspSerLeuThrAspLeuLeuA
GCGAGATGGTAGTACAATTGTCAGACAGCTTGACTGATCTTCTGG   495

                              70
spLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI
ACAAGTTTTCAAATATTTCTGAAGGCTTGAGTAATTATTCCATCA   540

         80                                 90
leAspLysLeuValAsnIleValAspAspLeuValGluCysValL
TAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTGA   585

             96
ysGluAsnSerSerLys
AAGAAAACTCATCTAAGGTAACTTTGTGTTCATTGGGATTATTTT   630

TCATTACGCTTCTCTAAAAACCCATGCTTCTTGGTGCTGTTGGGG   675

AAAATGAGGCACCTTTATTTATGATATTTTGATTGTATAAACTTC   720

AAATTTAAAAATCTTGTTCAGATGAGCAAAGAAAACAAGTATTTG   765

CAGTTATACTGCAATACTGAAGTGCACATTC   796
```

FIG.15B CONT.'

Intervening sequence of unknown length

```
TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCACTGGGATCA   45

CTACCCTGCATTACCAATCTGAATTACATACGTTAAAACAGCCAT   90

CTAAAAGTGCTAGTTGTAAGAGTCTAAATACTTGAATCTTTGAGA   135

GACATATTTATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA   180

                                       97
                                       AspLeuLysL
CTATTTGAAAAATGTAATCCTATTTTTCTTCTAGGATCTAAAAA    225

                             110
ysSerPheLysSerProGluProArgLeuPheThrProGluGluP
AATCATTCAAGAGCCCAGAACCCAGGCTCTTTACTCCTGAAGAAT   270

                    120                        130
hePheArgIlePheAsnArgSerIleAspAlaPheLysAspPheV
TCTTTAGAATTTTTAATAGATCCATTGATGCCTTCAAGGACTTTG   315

                                  140
alValAlaSerGluThrSerAspCysValValSerSerThrLeuS
TAGTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAA   360

      148
erProGluLysA
GTCCTGAGAAAGGTAAGACATGTAAGCATTTCCAGTTCAAATGTA   405

AACAACAAACTTAAATCTTCCCTATGTAGTAAGAATCTACCTCTG   450

TGTTAAGCTGTAGCAAGATACATGCATGTACGTCTAATAAAAAAG   495

CAGATATCAATAGCACAGAAGAAA                        519
```

Intervening sequence of unknown length

FIG.15B CONT.'

```
CTCTATAACTCATACAAATCACCATATAACACTGACACATTATTG    45

               150                            160
          spSerArgValSerValThrLysProPheMetL
CTTTCTATTTAGATTCCAGAGTCAGTGTCACAAAACCATTTATGT    90

                            170
euProProValAlaAlaSerSerLeuArgAsnAspSerSerSerS
TACCCCCTGTTGCAGCCAGCTCCCTTAGGAATGACAGCAGTAGCA    135

  176
erAsnA
GTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCA    180

ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCT    225

ACATTTATTATTATTGATACTGTTCTGTTACTGTTATTCCTTTTA    270

TGGTCTTCTTGAGACTTAAGTTTGTAGAATTAAATTTCCCTAGAG    315

CTGGAGATAATGTTTAGAGAATTAGGCCAATAAATTT            352
```

FIG.15C

```
                   -25           -20
                    M  K  K  T  Q  T  W  I  L  T  C  I  Y  L  Q
AAGCTTGCCTTTCCTTATGAAGAAGACACAAACTTGGATTCTCACTTGCATTTATCTTCAG   61

-10                          1                          10
 L  L  L  F  N  P  L  V  K  T  E  G  I  C  R  N  R  V  T  N
CTGCTCCTATTTAATCCTCTCGTCAAAACTGAAGGGATCTGCAGGAATCGTGTGACTAAT   121

                          20                            30
 N  V  K  D  V  T  K  L  V  A  N  L  P  K  D  Y  M  I  T  L
AATGTAAAAGACGTCACTAAATTGGTGGCAAATCTTCCAAAAGACTACATGATAACCCTC   181

                          40                            50
 K  Y  V  P  G  M  D  V  L  P  S  H  C  W  I  S  E  M  V  V
AAATATGTCCCCGGGATGGATGTTTTGCCAAGTCATTGTTGGATAAGCGAGATGGTAGTA   241

                          60                            70
 Q  L  S  D  S  L  T  D  L  L  D  K  F  S  N  I  S  E  G  L
CAATTGTCAGACAGCTTGACTGATCTTCTGGACAAGTTTTCAAATATTTCTGAAGGCTTG   301

                          80                            90
 S  N  Y  S  I  I  D  K  L  V  N  I  V  D  D  L  V  E  C  V
AGTAATTATTCCATCATAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTG   361

                          100                           110
 K  E  N  S  S  K  D  L  K  K  S  F  K  S  P  E  P  R  L  F
AAAGAAAACTCATCTAAGGATCTAAAAAAATCATTCAAGAGCCCAGAACCCAGGCTCTTT   421
```

FIG.15C CONT.'

```
                              120                                   130
 T  P  E  E  F  F  R  I  F  N  R  S  I  D  A  F  K  D  F  V
ACTCCTGAAGAATTCTTTAGAATTTTTAATAGATCCATTGATGCCTTCAAGGACTTTGTA    481

                              140                                   150
 V  A  S  E  T  S  D  C  V  V  S  S  T  L  S  P  E  K  D  S
GTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAAGTCCTGAGAAAGATTCC    541

                              160                                   170
 R  V  S  V  T  K  P  F  M  L  P  P  V  A  A  S  S  L  R  N
AGAGTCAGTGTCACAAAACCATTTATGTTACCCCCTGTTGCAGCCAGCTCCCTTAGGAAT    601

                              180      183
 D  S  S  S  S  N  S  K  Y  I  Y  L  I
GACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCAAT    661

TAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCTACATTTATTATTATTGA    721

TACTGTTCTGTTACTGTTATTCCTTTTATGGTCTTCTTGAGACTTAAGTTTGTAGAATTA    781

AATTTCCCTAGAGCTGGAGATAATGTTTAGAGAATTAGG                         820
```

FIG. 15D

```
GAGCTCCGAGCcCTCtCTGGCGCgCgAGGTATTTCGTCTGTnCCCGGGGGTGCCAGGTGA    60

GCCCCAGCGGATCCGGGAGGGTAAGCTGGGACTCCTCGCGAGCAGTAGCTGCAGGGTACC   120

AAGCTTCGCCCTCTGCGTCCCCGCGCCTTCGCGGTCTCCCGCCAGTGCAGGTCCGGGGCC   180

CCCAGGCGAGCGGACAAGGTTGGCCTAATCTGCCAAACTTCTGGGGCATTTACCGTGCTC   240

TGGCCGCCCTCCCGATTCTTCCCTCCGCGCCCTTGCCTGCTTCTCGCCTACCCCGGGCTC   300

CGGAAGGGAAGGAGGCGTGTCCGGAGCAGGCGGGCGGGAACTGTATAAAAGCGCCGGCGG   360

CTCAGCAGCCGGCTTCGCTCGCCGCCTCGCGCCGAGACTAGAAGCGCTGCGGGAAGCAGG   420

GACAGTGGAGAGGGCGCTGCGCTCGGGCTACCCAATGCGTGGACTATCTGCCGCCGCTGT   480

TCGTGCAAT[illegible]CGCTGGAGCTCCAGAACAGCTAAACGGAGTCGCCACACCACTGTTTGTGC   540

                                 -25            -21
                                 MetLysLysThrGln
TGGATCGC[illegible]GCTGCCTTTCCTTATGAAGAAGACACAAGTGAGTAGGGCGCGCCCGGGA   600

GCTCCCAGGCTCTCCAGGAAAAATCGCGCCCGGTGCCCCGGGGAAGCCGGCGCTCCCTGG   660

GACTTGCAGCTGGGGCGTGCAGGGCTGTGCCTGCCGGGTGAGACAAGAGGATGCGGGGGA   720

GGCCGGCGTGGTGTGTGATCCCGAGCCGAGCCGnnTGAGCCAGGGAGAAAAGGAGTGGGA   780

GTnCTGAGAGGGAGCCAGTGTCAAGTTTGGAGCCTCAGCAGTTAAGTTTTGAGCTGTCAG   840

TCGGAAACCGTAATTCCCGTCTGGTGGAAAGATTGGCTTTTnGnCCACGGAATGTAAGTT   900

ATCAC                                                          905
```

Intervening sequence of unknown length

```
AGATACTACAAAGATAAATCAGTTGCACAAGTTCTTGAAACTCTACAGTGTAATAAGGAA   60

AAATAAGTCATGCATAAAAGCAACTATAATACATAATAGAAAATGTTATTTTCAAGCCGA   120

TGTGTAGGTTATGTGTGTTCGAGAGAGAGAGAGAGAAGACAGATTACTTTCTGCTAGGGT   180

TCAAGAATGCCTTCCTGTTGGCTAAGGAAATATTTTCCTTAAGTGGCTAAAAAGCTGTGT   240

TTCAAAATATTCTTTTGATGTCTCACAAATTCAGTGGAATTCTCTTAGGTCTAAAAATAT   300

ACATCTCTCTCACTTTAACTTGGTGTGCTATTGTAGATTATTGGATTAAAGCACTGCTCA   360

GGGATTATGCTGCTTCTTGCCAAGCAGTCTACATTTAAAGTAGAAATAAGATGTTTCTTT   420

TGGTGCCATAAGGTATACATTTTATGCATTCTCTAGTTTTTAGAAGATACCCTAAGGGCT   480

AAGTCTTTAACATGCTGCTACAAGTTTATTCCTAATTGCCATTGGGAAATTGGCTGAAGA   540

AAGTTTTTAACAAAAGTTAACAATATTGTCATTGAGAGAATAATTCAAAATGGATTTTAA   600

CTAAAAGCTTTTAAAAACTTTGGTGAGCATAGCTTGAATGCGTAATATTTAATTGCATTT   660

AAGCCAATAACATATATTAGACTGGTCTTTTTGTGCATCAAGGCATTAGATGTTAAAAGT   720

                                                         -20
                                                          Th
TTGAATGATTACAGATCTTAACTGATGATCACCAAGCAATTTTTCTGTTTTCATTTAGAC   780

                   -10
rTrpIleLeuThrCysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrGl
TTGGATTCTCACTTGCATTTATCTTCAGCTGCTCCTATTTAATCCTCTCGTCAAAACTGA   840
```

FIG. 15D CONT.

FIG. 15D CONT.

```
1                  10                 18
uGlyIleCysArgAsnArgValThrAsnAsnValLysAspValThrLysLeu
AGGGATCTGCAGGAATCGTGTGACTAATAATGTAAAAGACGTCACTAAATTGGTAAGTAA   900

GGAATGCTTTACCGTGCTGTGTAAAAAAGAGCTGTGGCTCTTTTTCCTGTGCTTGTTGAT   960

AAAAGATTTAGATTTTTCTTGCCCCAAAGTAATGTTTTCCTAAAGTGGGAAAGTAATCA   1020

CTGGGTTACAATAAAGGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA  1080

TTTGTTGGTAAAACTGGCTAGTTGCACACCACTGCTGTGACTGCTTCTTTGCTGGTCTTC  1140

TCCCCATCCTTCATAGGCAGTGAAGGACCTTGGAGAGTTCGCTGTGTGCTGATGGGCTTG  1200

CCCCAGCTTGTTCCCCATAATCTCTCCAGTGGGTTTCCCAGCATGTTCTATTCCCCTTCA  1260

CATGTCTTCCTACTCTTCTTTAAAAAGCCTAACGAAAGGAAATCTGAAATGGCTATTCTC  1320

CCAATTCAATCAGCAGGAAGACCCTGTCACATGTCAGTGGGTGTTTGCTCCTTCAGGGAA  1380

CATAGAGAGGTGATTCATTGCCCACATGTTGAAGGGACTCATCTCCCTGGTTTGTCACAT  1440

TGAACTCTTCCCTCAGCGAAAGCATTTGCATTGCTTCCC                       1479
```

Intervening sequence of unknown length

```
GAATTCCAAGATCACAGGTGGAAGGTGAAATTCAGATCATGTTTCCAAAACTCAGTAGGT  60

TATACCTAGCCAGGCATAACTGAATTTGGAGTCTAAAAGATCTGTATTATCACTTTTTTA  120

TTTTGAAGGATGCCTTTTGATTACAGAGGGAAATCAAGGATTAAAAATCAATATACATGT  180
```

```
AAATATTGAAATTCATTGGTAACTTTAAAAAGCACAACAGTTTTGTGTGCTTTTCTCCAA   240

AGCACTACAAATATGATTAATTGATGTATAAGAATTTTCTTATGGAATTTTTTTTTTTGT   300

             19                                              30
             ValAlaAsnLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM
CTCTGTAGGTGGCAAATCTTCCAAAAGACTACATGATAACCCTCAAATATGTCCCCGGGA   360

             39
etAspValLeu
TGGATGTTTTGGTATGTAAACTACATTTCTGAGTTTCATTTTAGTAGCTCATAGAAGAAA   420

TGGGATCATTCATATTGAGATAGTACACTAGCTGCTATTTAGGAGCTTGCTTATTGTCAG   480

GATTTGAAGAATTTATCTTTGGAATTTGACTTGCAGGCTTTTTTTTCCCCCTCTT        535
```

Intervening sequence of unknown length

```
CCTGTTACAAGAGTCCCTCCTCCTATTACAATAGTCCCTCCTCCTCCTGTCACACTAGTC   60

CCTTCTCTTCCTGTTACAATAACCCCTGTCCTCCTATTACAACATTTTAAGTAATGTAAT   120

ATTAATTTTAAAAATCTGGCCAGGCACGGTGGTTCATGCTTGTAATCCCAGCACATTGGG   180

AAGCTGAGACGGGTGGATCATTTGAGGTCAGGAAGTTTGAGACAGCCTGGCCAACATGGT   240

GAAACTTCCTCTCTACTAAAAATAAAAAAGTAGCCAGGCATGGTGGCAGGCACTTGTAAT   300

CTGAGCTACTCGAGAGGCTGAGGCAGGAGAATCACTTGAGTAACTAAAACGATAGCTTTG   360

AAGAGTACTCCGAGTTTTATGGCACTTACTTATTAAAATAGCTGTTTTGTCTCTTTTTTC   420
```

FIG. 15D CONT.

FIG. 15D CONT

```
            40                                  50
         ProSerHisCysTrpIleSerGluMetValValGlnLeuSerAspSerL
ATATCTTGCAGCCAAGTCATTGTTGGATAAGCGAGATGGTAGTACAATTGTCAGACAGCT   480

            60                                  70
euThrAspLeuLeuAspLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI
TGACTGATCTTCTGGACAAGTTTTCAAATATTTCTGAAGGCTTGAGTAATTATTCCATCA   540

            80                                  90
leAspLysLeuValAsnIleValAspAspLeuValGluCysValLysGluAsnSerSerL
TAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTGAAAGAAAACTCATCTA   600
96
ys
AGGTAACTTTGTGTTCATTGGGATTATTTTTCATTACGCTTCTCTAAAAACCCATGCTTC   660

TTGGTGCTGTTGGGGAAAATGAGGCACCTTTATTTATGATATTTTGATTGTATAAACTTC   720

AAATTTAAAAATCTTGTTCAGATGAGCAAAGAAAACAAGTATTTGCAGTTATACTGCAAT   780

ACTGAAGTGCACATTC                                               796

                        Intervening sequence of unknown length

TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCACTGGGATCACTACCCTGCATTACC   60

AATCTGAATTACATACGTTAAAACAGCCATCTAAAAGTGCTAGTTGTAAGAGTCTAAATA   120

CTTGAATCTTTGAGAGACATATTTATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA   180

                                      97
                                    AspLeuLysLysSerPheLysSerP
CTATTTGAAAAATGTAATCCTATTTTTTCTTCTAGGATCTAAAAAAATCATTCAAGAGCC   240
```

FIG. 15D C

```
                110                                     120
roGluProArgLeuPheThrProGluGluPhePheArgIlePheAsnArgSerIleAspA
CAGAACCCAGGCTCTTTACTCCTGAAGAATTCTTTAGAATTTTTAATAGATCCATTGATG    300

                130                                     140
laPheLysAspPheValValAlaSerGluThrSerAspCysValValSerSerThrLeuS
CCTTCAAGGACTTTGTAGTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAA    360

        148
erProGluLysA
GTCCTGAGAAAGGTAAGACATGTAAGCATTTCCAGTTCAAATGTAAACAACAAACTTAAA    420

TCTTCCCTATGTAGTAAGAATCTACCTCTGTGTTAAGCTGTAGCAAGATACATGCATGTA    480

CGTCTAATAAAAAAGCAGATATCAATAGCACAGAAGAAACTAATGATTGTAGATTTGTGGG   541


                  Intervening sequence of unknown length


                                                         spS
CTCTATAACTCATACAAATCACCATATAACACTGACACATTATTGCTTTCTATTTAGATT    60

150                                     160
erArgValSerValThrLysProPheMetLeuProProValAlaAlaSerSerLeuArgA
CCAGAGTCAGTGTCACAAAACCATTTATGTTACCCCCTGTTGCAGCCAGCTCCCTTAGGA    120

170                  176
snAspSerSerSerSerAsnA
ATGACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCA    180

ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCTACATTTATTATTATT    240

GATACTGTTCTGTTACTGTTATTCCTTTTATGGTCTTCTTGAGACTTAAGTTTGTAGAAT    300
```

```
TAAATTTCCCTAGAGCTGGAGATAATGTTTAGAGAATTAGGCCAATAAATTTTCTGCTGA   360

GGTTATTTTAAATAAGACATAAAATTAATTTTAGAAATATGATTTATGCCTTTTGTTGAA   420

TCATTAACATATAT                                                 434

          Intervening sequence of unknown length

ACAGAAACAGTTAAAACAACCACAGCATAAGAGnAAAACTTCTAGAATGGATATGCTGTA   60

                          178
                        rgLysAlaLysAsnProProGlyAspSerSerL
TTCATCAGTGTGTTCTTTAAATTATAGGGAAGGCCAAAAATCCCCCTGGAGACTCCAGCC   120

    190                            200
euHisTrpAlaAlaMetAlaLeuProAlaLeuPheSerLeuIleIleGlyPheAlaPheG
TACACTGGGCAGCCATGGCATTGCCAGCATTGTTTTCTCTTATAATTGGCTTTGCTTTTG   180

         213
lyAlaLeuTyrTrpLys
GAGCCTTATACTGGAAGGTAAGTGGTACCATTCCTTtTTTTAAAAATATGCTATGTtTAC   240

ATAAATTATCATCTTTTTTTCCTCAAGAAATGATCCTTtAAGAAAACAGTGAATCTACCT   300

TAGCTTATACTAAACAAAATTTAAATTTTATAAAGTTTCCTGTTTCTCATTATGTCTGGA   360

GACAATCCCTCTAGCTGATAATTCACGCTTAAGAATTAGGAACT                   404

          Intervening sequence of unknown length
```

FIG. 15D CONT.

FIG. 15D CONT

```
AAAACTGTTATTGGAGTTATTGCCATAAAAGATAAAAGTGGAGTCCACTTACCTCTTAAA   60
                                                         214
                                                         LysArgG
TATTAGACCATTCATTGATTATTTTACAGTATATGTCTTTCTTCTTTTTCCAGAAGAGAC   120

       220                                  230        235
lnProSerLeuThrArgAlaValGluAsnIleGlnIleAsnGluGluAspAsnGluIleS
AGCCAAGTCTTACAAGGGCAGTTGAAAATATACAAATTAATGAAGAGGATAATGAGATAA   180

e
GGTATTTTGTTTTGCTAAATGTGTgCCCAATCAAGCATGACATTGCCATTTCACACACTG   240

TGTACCTGCCCATAATGTCTTTAAGAAGTCCTTCACTCATGACAGTAGCTCCTAACCAGT   300

GAGTCCCAACTCTATCCATGTTTCTGATGTCTCACTCTCTCTTC                   344

              Intervening sequence of unknown length

GTATGTGTATATGCATATACAGAGAAAGAAATGTTTTAACTACTTGGAAAGACTACCTTA   60

AGACAAATGAAGTCTTCCCTCTTCCCTATAGTAATAAGAAGGTAGGCTCCCCCATTCAAT   120

TTTGCAATCTTCTGCTACTATATTTACAGAAAAGCTGCCTTTTACAATGCCGAGATCATG   180

                                                          rM
GTGTACCTCAGAATCTCTGACCAAGAGCAAATAAGCATTTtTTCTTATTGTTTTTCAGTA   240

237                     248
etLeuGlnGluLysGluArgGluPheGlnGluVal
TGTTGCAAGAGaAAGAGAGAGAGTTTCAAGAAGTGTAATTGTGGCTTGTATCAACACTGT   300

TACTTTCGTACATTGGTAAGTTTTTTTCTTCTTTCCTTTTTTTTTCTTTTTTTTATTATA   360
```

FIG. 15D CONT.

CTTTAAGTTCTAGGGTACATGTGCACAATGTGCAGGTTTGTTACGTATGTTTACATGTGC 420

CATGTT 426

FIG.16A

```
           -25                                                        25
Human      MKKTQTWILT CIYLQLLLFN PLVKTEGICR NRVTNNVKDV TKLVANLPKD
Monkey     MKKTQTWILT CIYLQLLLFN PLVKTEGICR NRVTNNVKDV TKLVANLPKD
Dog        MKKTQTWIIT CIYLQLLLFN PLVKTKGICG KRVTDDVKDV TKLVANLPKD
Cat        MKXTQTWIVT CIYLQXLLFN PLVKTKGLCR NRVTDDVKDV TKLVANLPKD
Cow        MKKTQTWIIT CIYLQLLLFN PLVHTQGICS NRVTDDVKDV TKLVANLPKD
Rat        MKKTQTWIIT CIYLQLLLFN PLVKTQEICR NPVTDNVKDI TKLVANLPND
Mouse      MKKTQTWIIT CIYLQLLLFN PLVKTKEICG NPVTDNVKDI TKLVANLPND
Chicken         TWIIT CFCLQLLLLN PLVKAQSSCG NPVTDDVNDI AKLVGNLPND
Scfpep     MKkTQTWIiT CiyLQlLLfN PLVkt.giCr nrVTd.VkDv tKLVaNLPkD

           26                                                         72
Human      YMITLKYVPG MDVLPSHCWI SEMVVQLSDS LTDLLDKFSN ISEG...LSN
Monkey     YMITLKYVPG MDVLPSHCWI SEMVVQLSDS LTDLLDKFSN ISEG...LSN
Dog        YKIALKYVPG MDVLPSHCWI SVMVEQLSVS LTDLLDKFSN ISEG...LSN
Cat        YKIALKYVPG MDVLPSHCWI SVMVEQLSVS LTDLLDKFSN ISEG...LSN
Cow        YMITLKYVPG MDVLPSHCWI SEMVEQLSVS LTDLLDKFSN ISEG...LSN
Rat        YMITLNYVAG MDVLPSHCWL RDMVTHLSVS LTTLLDKFSN ISEG...LSN
Mouse      YMITLNYVAG MDVLPSHCWL RDMVIQLSLS LTTLLDKFSN ISEG...LSN
Chicken    YLITLKYVPK MDSLPNHCWL HLMVPEFSRS LHNLLQKFSD ISDMSDVLSN
Scfpep     YmItLkYVpg MDvLPsHCWi seMVeqlSvS LtdLLdKFSn ISeg...LSN

           73                                                        121
Human      YSIIDKLVNI VDDLVECVKE NSSKD.LKKS FKSPEPRLFT PEEFFRIFNR
Monkey     YSIIDKLVNI VDDLVECVKE NSSKD.LKKS FKSPEPRLFT PEEFFRIFNR
Dog        YSIIDKLVKI VDDLVECTEG YSFEN.VKKA PKSPELRLFT PEEFFRIFNR
Cat        YSIIDKLVKI VDDLVECVEG HSSEN.VKKS SKSPEPRLFT PEEFFRIFNR
Cow        YCIIDKLVKI VDDLVECMEX HSSEN.VKKS SKSPEPRQFT PEKFFGIFNK
Rat        YSIIDKLGKI VDDLVACMEE NAPKN.VKES LKKPETRNFT PEEFFSIFNR
Mouse      YSIIDKLGKI VDDLVLCMEE NAPKN.IKES PKRPETRSFT PEEFFSIFNR
Chicken    YSIINNLTRI INDLMACLAF DKNKDFIKEN GHLYEEDRFI PENFFRLFNS
Scfpep     YsIIdkLvkI vdDLveC.ee nsskn.vKks .kspEprlFt PEeFFriFNr
```

FIG.16B

	122				169
Human	SIDAFKDF.V	VASETSDCVV	SSTL.SPEKD	SRVSVTKPFM	LPPVAASSLR
Monkey	SIDAFKDF.A	VASETSDCVV	SSTL.SPEKD	SRVSVTKPFM	LPPVAASSLR
Dog	SIDAFKDLET	VASKSSECVV	SSTL.SPDKD	SRVSVTKPFM	LPPVAASSLR
Cat	SIDAFKDLEM	VASKTSECVV	SSTL.SPEKD	SRVSVTKPFM	LPPVAASSLR
Cow	SIDAFKDLEI	VASKMSECVI	SSTS.SPEKD	SRVSVTKPFM	LPPVAASSLR
Rat	SIDAFKDF.M	VASDTSDCVL	SSTL.GPEKD	SRVSVTKPFM	LPPVAASSLR
Mouse	SIDAFKDF.M	VASDTSDCVL	SSTL.GPEKD	SRVSVTKPFM	LPPVAASSLR
Chicken	TIEVYKEFAD	SLDK.NDCIM	PSTVETPEND	SRVAVTKTIS	FPPVAASSLR
Scfpep	sIdafKdf.m	vasktsdCvv	sSTl.sPekD	SRVsVTKpfm	lPPVAASSLR

	170				213
Human	NDSSSSNRKA	KNPPGD....	..SSLHWAAM	ALPALFSLII	GFAFGALYWK
Monkey	NDSSSSNRKA	KNPTGD....	..SSLHWAAM	ALPAFFSLII	GFAFGALYWK
Dog	NDSSSSNRKA	SNSIGD....	..SNLQWAAM	ALPAFFSLVI	GFAFGALYWK
Cat	NDSSSSNRKX	TNPIED....	..SSIQWAVM	ALPACFSLVI	GFAFGAFYWK
Cow	NDSSSSNRKA	SNSIED....	..SSLQWAAV	ALPAFFSLVI	GFAFGAFYWK
Rat	NDSSSSNRKA	AKSPED....	..PGLQWTAM	ALPALISLVI	GFAFGALYWK
Mouse	NDSSSSNRKA	AKAPED....	..SGLQWTAM	ALPALISLVI	GFAFGALYWK
Chicken	NDSIGSNTSS	NSNKEALGFI	SSSSLQGISI	ALTSLLSLLI	GFILGAIYWK
Scfpep	NDSssSNrka	.n..ed....	..sslqwaam	ALpalfSLvI	GFafGAlYWK

	214			248
Human	KRQPSLTRAV	ENIQIN...E	EDNEISMLQE	KEREFQEV
Monkey	KRQPSLTRAV	ENIQIN...E	DDNEISMLQE	KEREFQEV
Dog	KKQPNLTRTV	ENIQIN...E	EDNEISMLQE	KEREFQEV
Cat	KKQPNLTRTV	ENIQIN...E	EDNEISMLQE	KEREFQEV
Cow	KKQPNLTRTV	ENRQIN...E	EDNEISMLQE	KEREFQEV
Rat	KKQSSLTRAV	ENIQIN...E	EDNEISMLQQ	KEREFQEV
Mouse	KKQSSLTRAV	ENIQIN...E	EDNEISMLQQ	KEREFQEV
Chicken	KTHPKSRPES	NETIQCHGCQ	EENEISMLQQ	KEKEHLQV
Scfpep	Kkqpsltrav	eniqin...e	edNEISMLQe	KErEfqeV

FIG. 16C

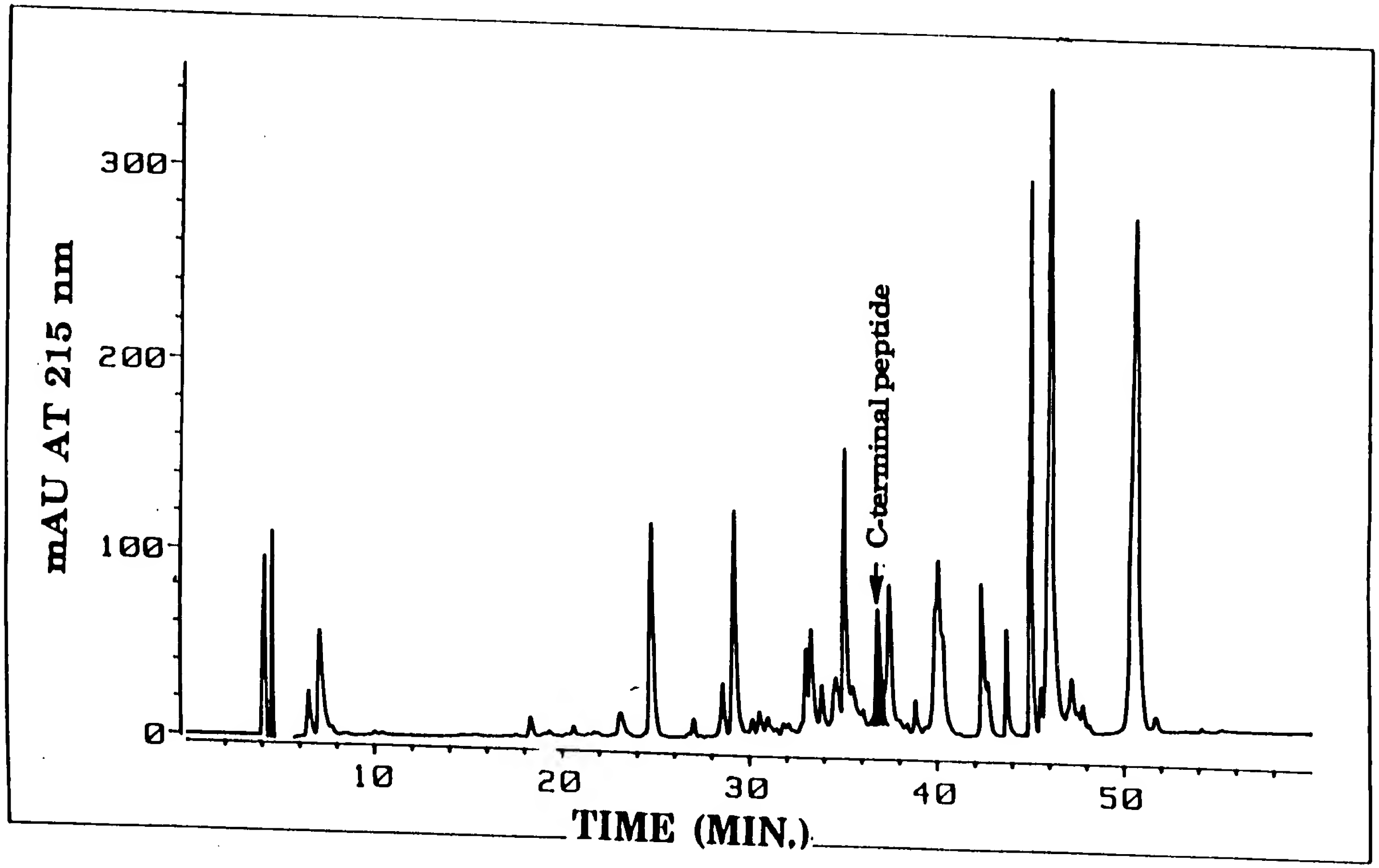

mAU AT 215 nm
300
200
100
0
10
20
30
40
50
TIME (MIN.)
C-terminal peptide

FIG. 16D

EcoRI

```
        ta  a   t   t   t a a       t   t   c       g       t   a
GAATTCTTCCGTATCTTCAACCGTTCCATCGACGCTTTCAAAGACTTCGTT
E   F   F   R   I   F   N   R   S   I   D   A   F   K   D   F   V

  g   a   t       ta gt   t   t   g       t   a   at a ag   t   g
GTTGCTTCCGAAACCTCCGACTGCGTTGTTTCCTCCACCCTGTCTCCGGAA
V   A   S   E   T   S   D   C   V   V   S   S   T   L   S   P   E
```

BstEII

```
      t     a a   ca gt   c   a       a   t   t a   c   t  .  a
AAAGACTCCCGTGTTTCGGTTACCAAACCGTTCATGCTGCCGCCGGTTGCT
K   D   S   R   V   S   V   T   K   P   F   M   L   P   P   V   A

  c ag        t a  g   t    ag  ag t ag  ag t   tag t   g     a   t
GCTTCCTCCCTGCGTAACGACTCCTCCTCCTCCAACTCCAAATACATCTAC
A   S   S   L   R   N   D   S   S   S   S   N   S   K   Y   I   Y
```

BamHI

```
      t
CTGATCTAATAGGATCC
L   I   *   *
```

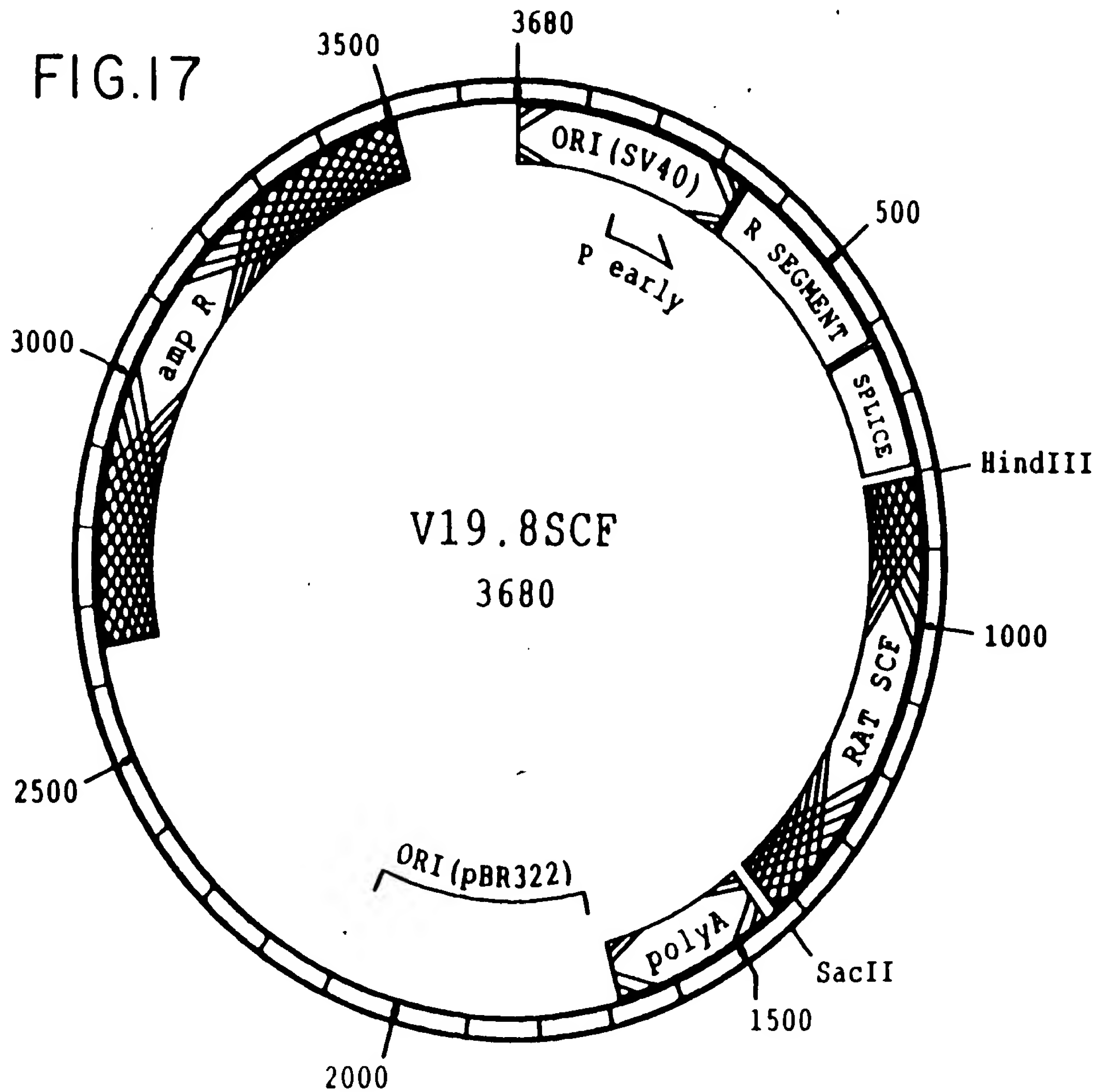
FIG 16E

BstEII   BamHI

<u>GGTTACC</u>AAACCGTTCATGCTGCCGCCGGTTGCTGCTTAATA<u>GGATCC</u>

V T K P F M L P P V A A * *

FIG.17



3680
3500
500
3000
2500
2000
1500
1000
HindIII
SacII
ORI (SV40)
P early
R SEGMENT
SPLICE
RAT SCF
polyA
ORI (pBR322)
amp R
V19.8SCF
3680

FIG.18

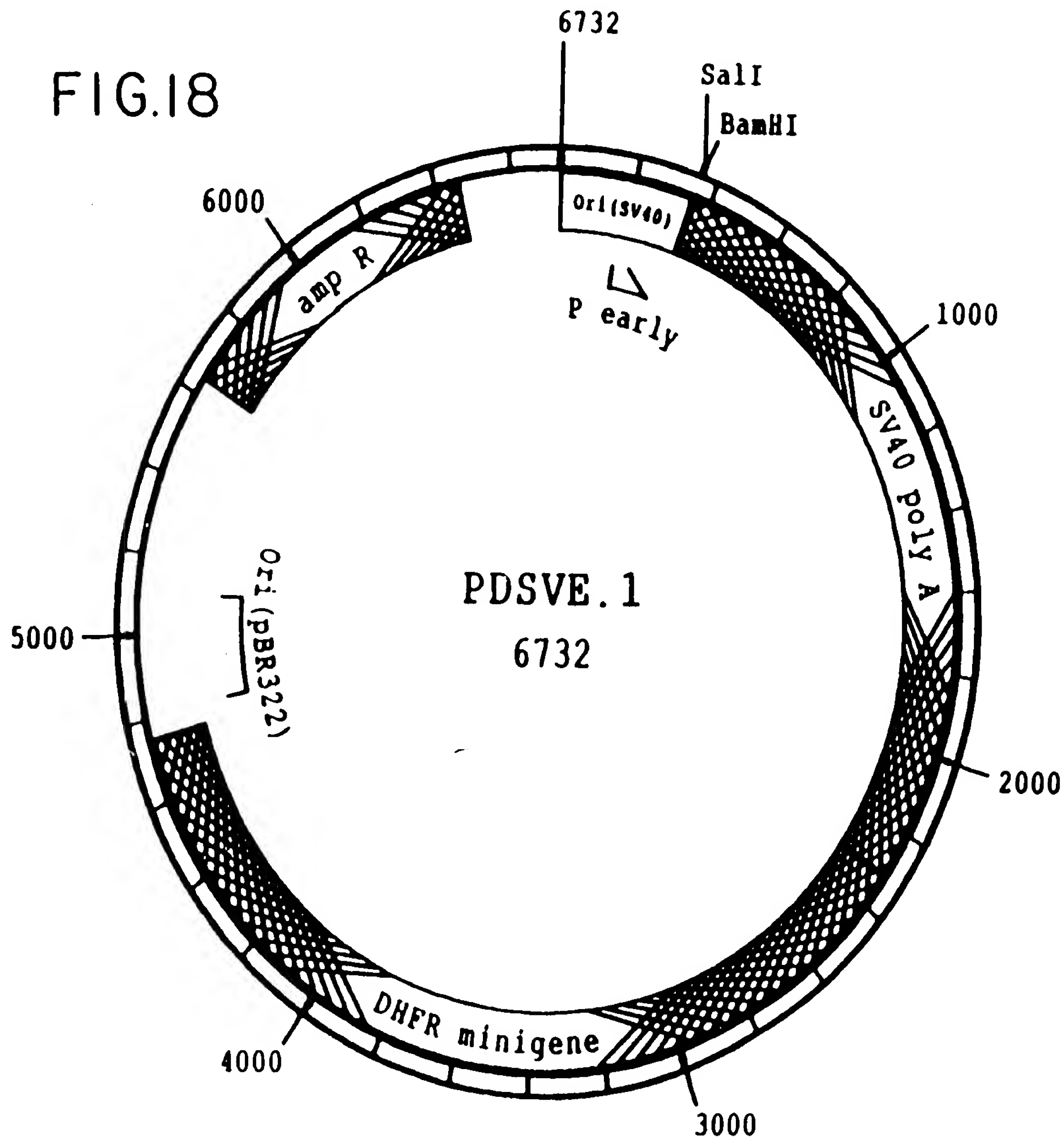
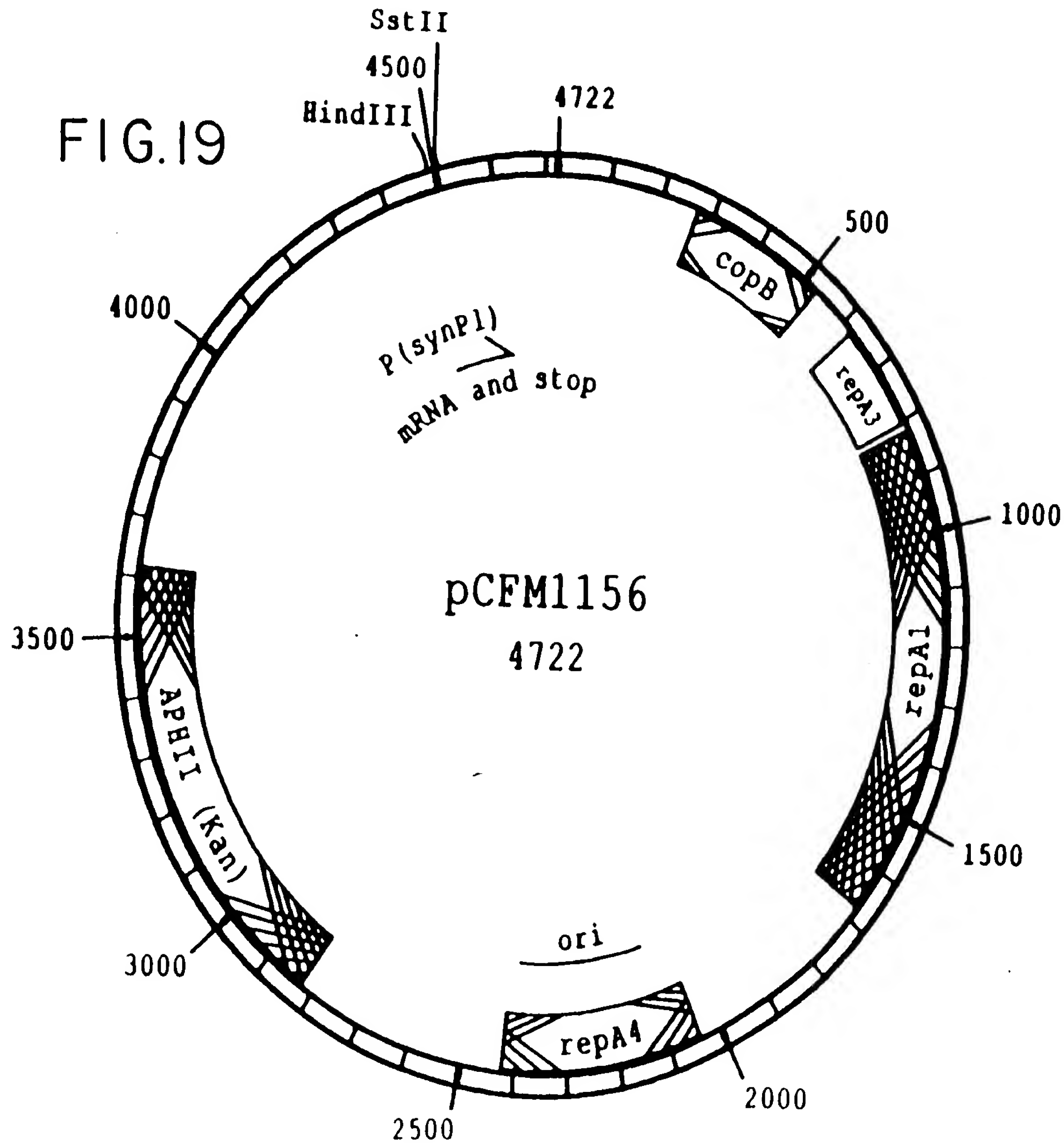
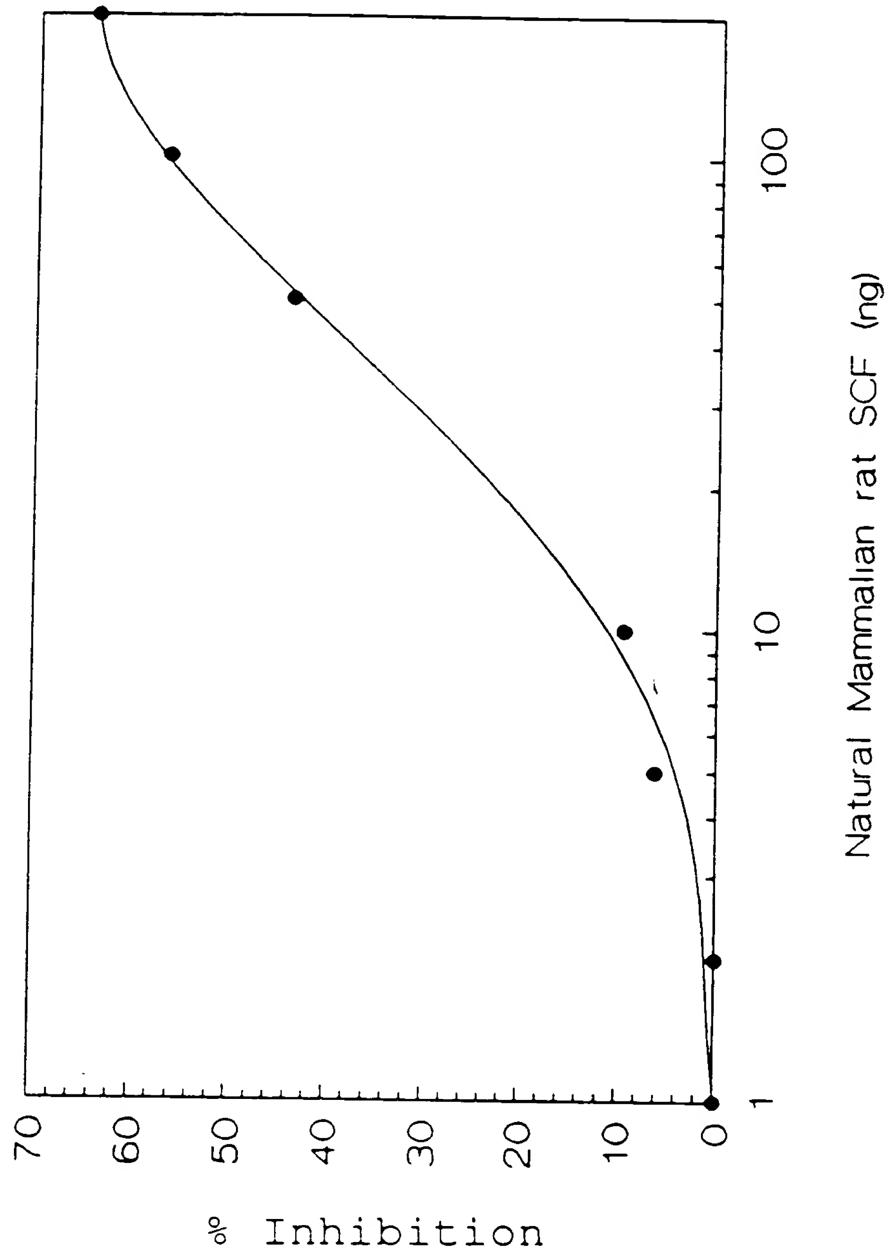

6732
SalI
BamHI
Ori(SV40)
P early
1000
SV40 poly A
2000
3000
DHFR minigene
4000
Ori (pBR322)
5000
6000
amp R
PDSVE.1
6732

FIG.19



SstII
4500
HindIII
4722
500
copB
repA3
1000
repA1
1500
2000
repA4
ori
2500
3000
APHII (Kan)
3500
4000
P(synP1)
mRNA and stop
pCFM1156
4722

FIG.20A



% Inhibition
0
10
20
30
40
50
60
70
Natural Mammalian rat SCF (ng)
1
10
100

FIG.20B

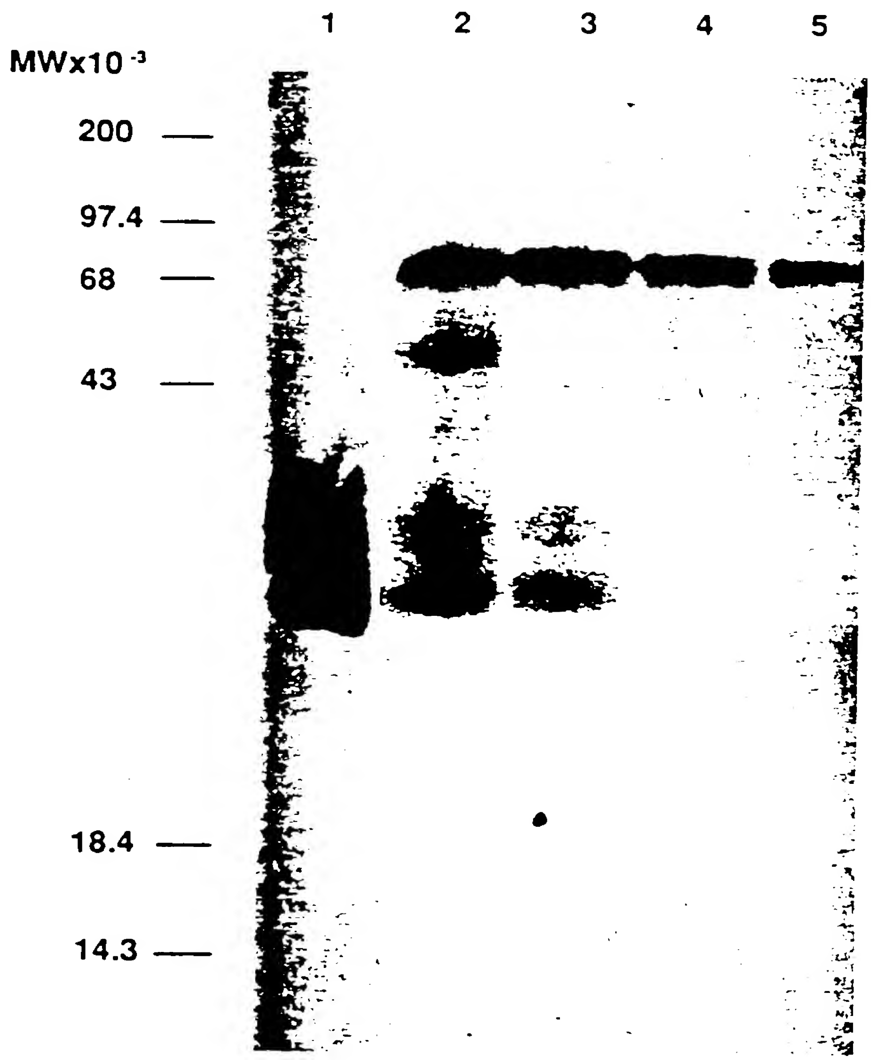


FIG. 21

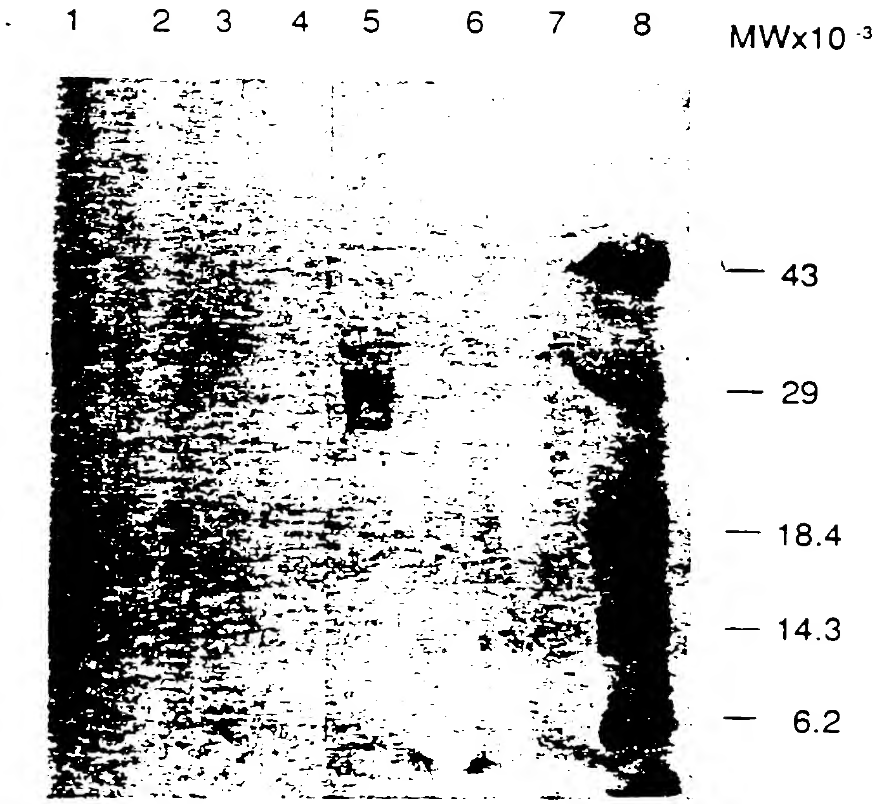


FIG.22

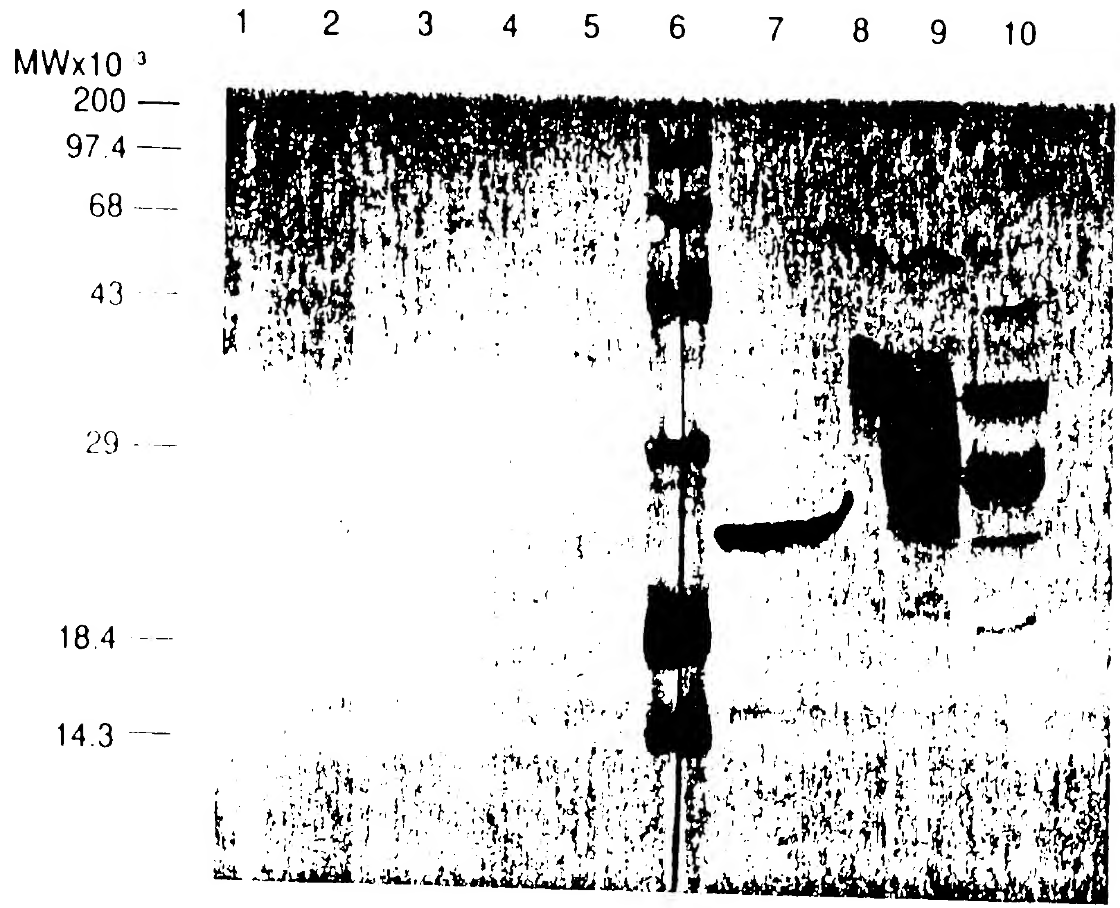
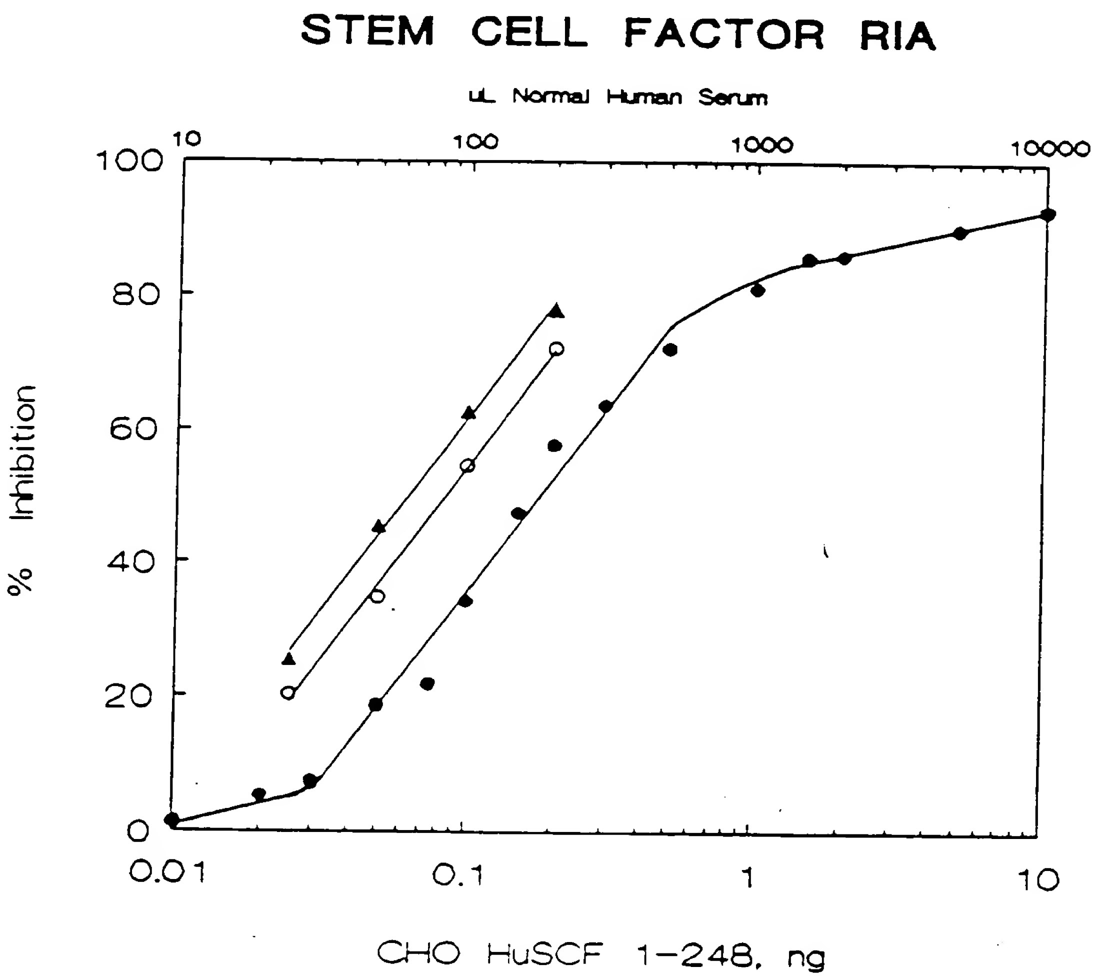
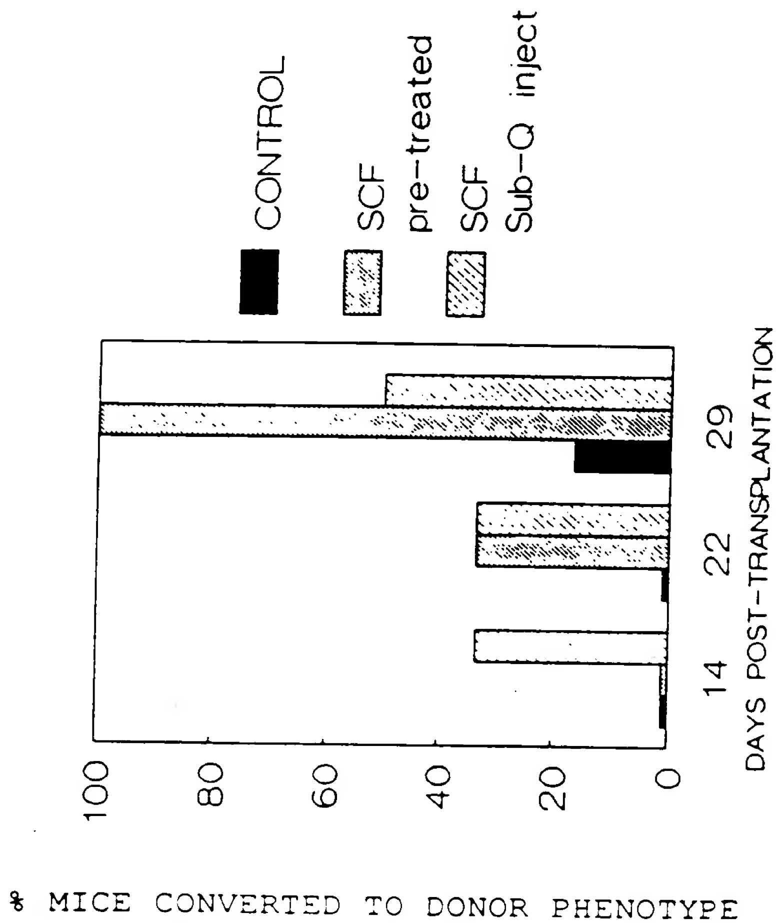


FIG. 22A



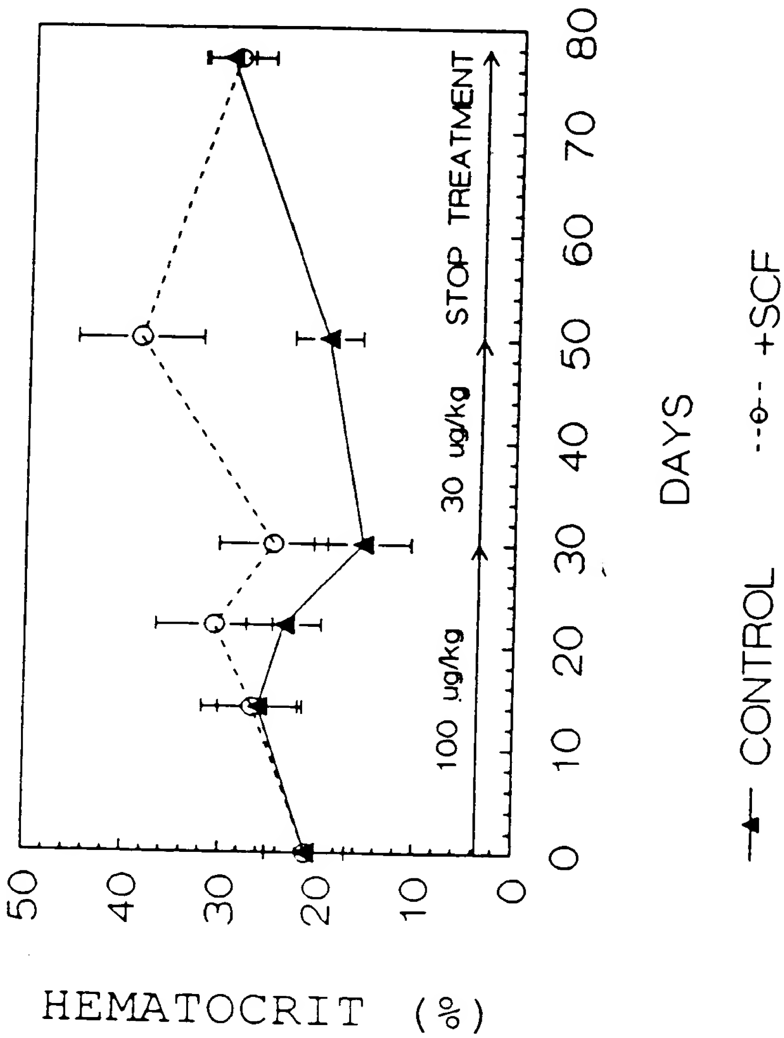
STEM CELL FACTOR RIA
uL Normal Human Serum
10
100
1000
10000
100
80
60
40
20
0
% Inhibition
0.01
0.1
1
10
CHO HuSCF 1-248, ng

FIG. 23



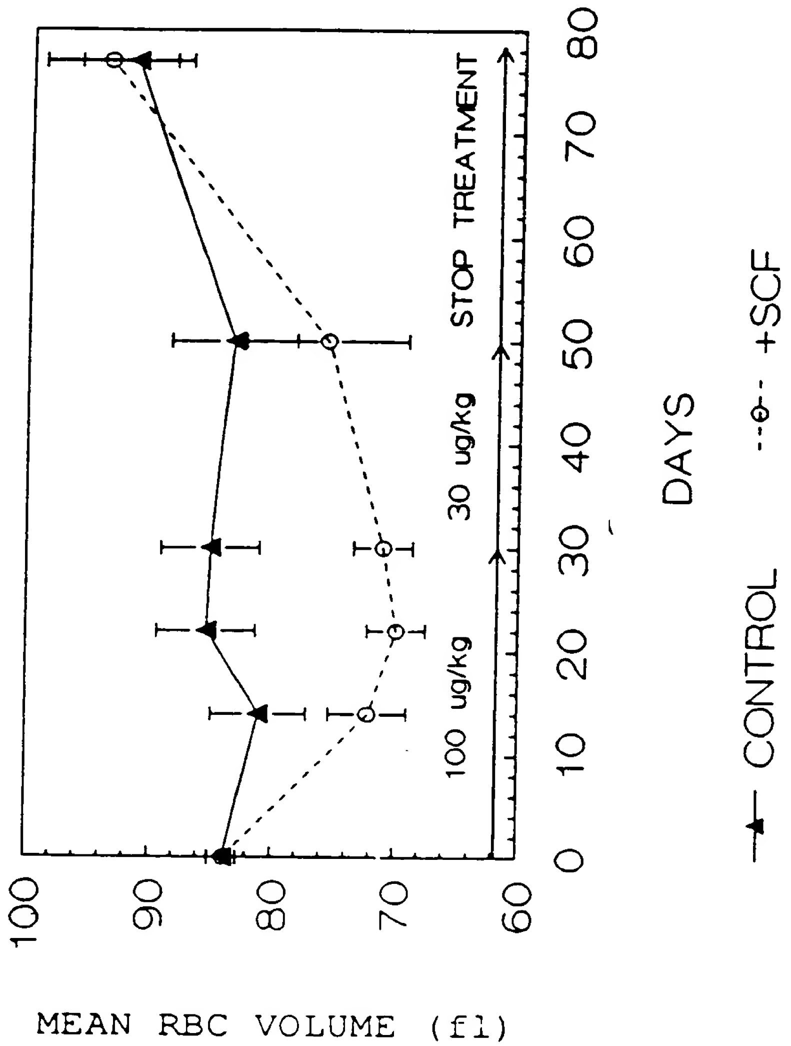
CONTROL
SCF pre-treated
SCF Sub-Q inject
100
80
60
40
20
0
14
22
29
DAYS POST-TRANSPLANTATION
% MICE CONVERTED TO DONOR PHENOTYPE

FIG. 24A



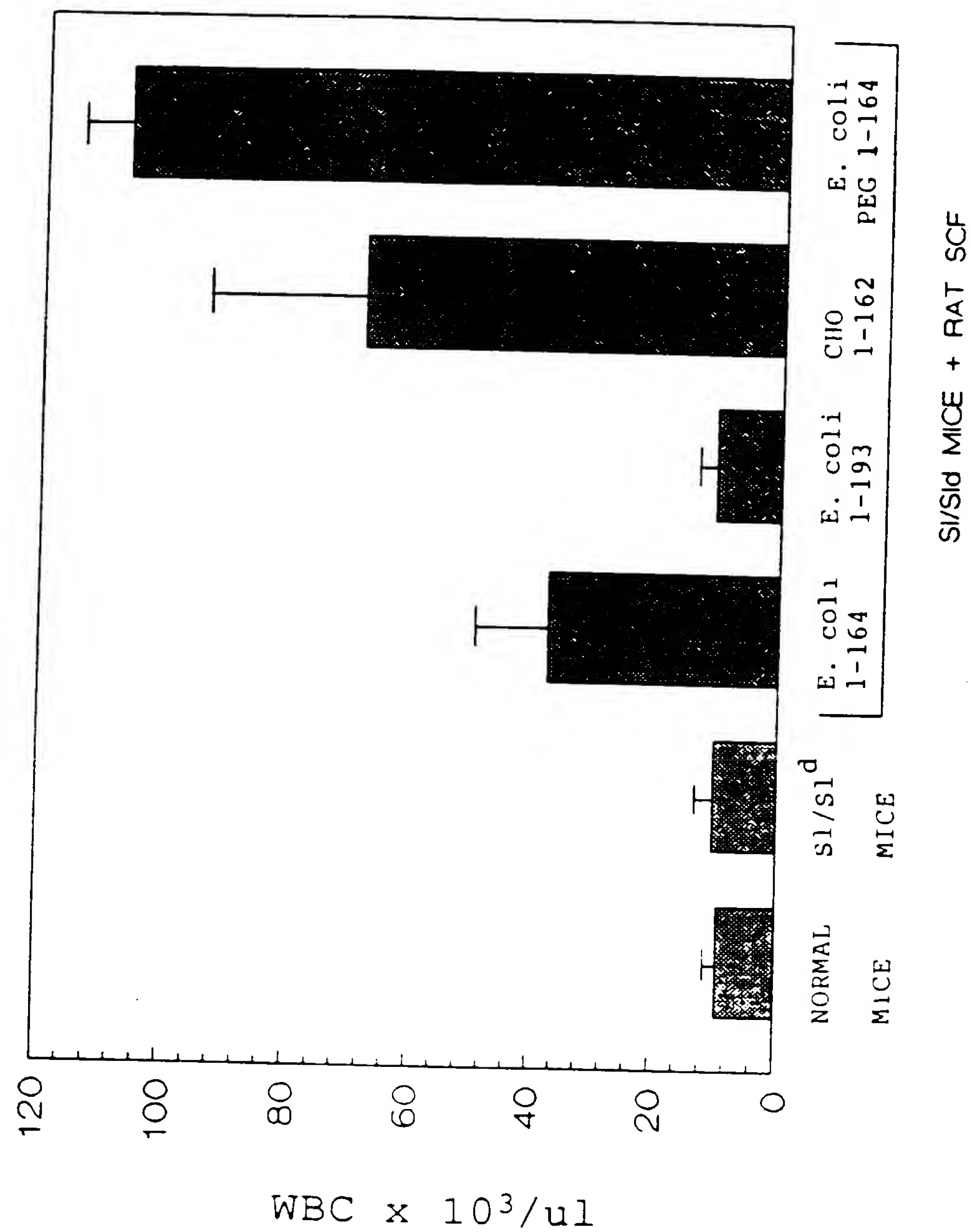
HEMATOCRIT (%)
0
10
20
30
40
50
DAYS
0
10
20
30
40
50
60
70
80
100 ug/kg
30 ug/kg
STOP TREATMENT
CONTROL
+SCF

FIG. 24B



100
90
80
70
60
MEAN RBC VOLUME (fl)
0
10
20
30
40
50
60
70
80
DAYS
100 ug/kg
30 ug/kg
STOP TREATMENT
CONTROL
+SCF

FIG. 25



WBC x 10³/ul
0
20
40
60
80
100
120
NORMAL MICE
Sl/Sl^d MICE
E. coli 1-164
E. coli 1-193
CHO 1-162
E. coli PEG 1-164
Sl/Sld MICE + RAT SCF

FIG. 26

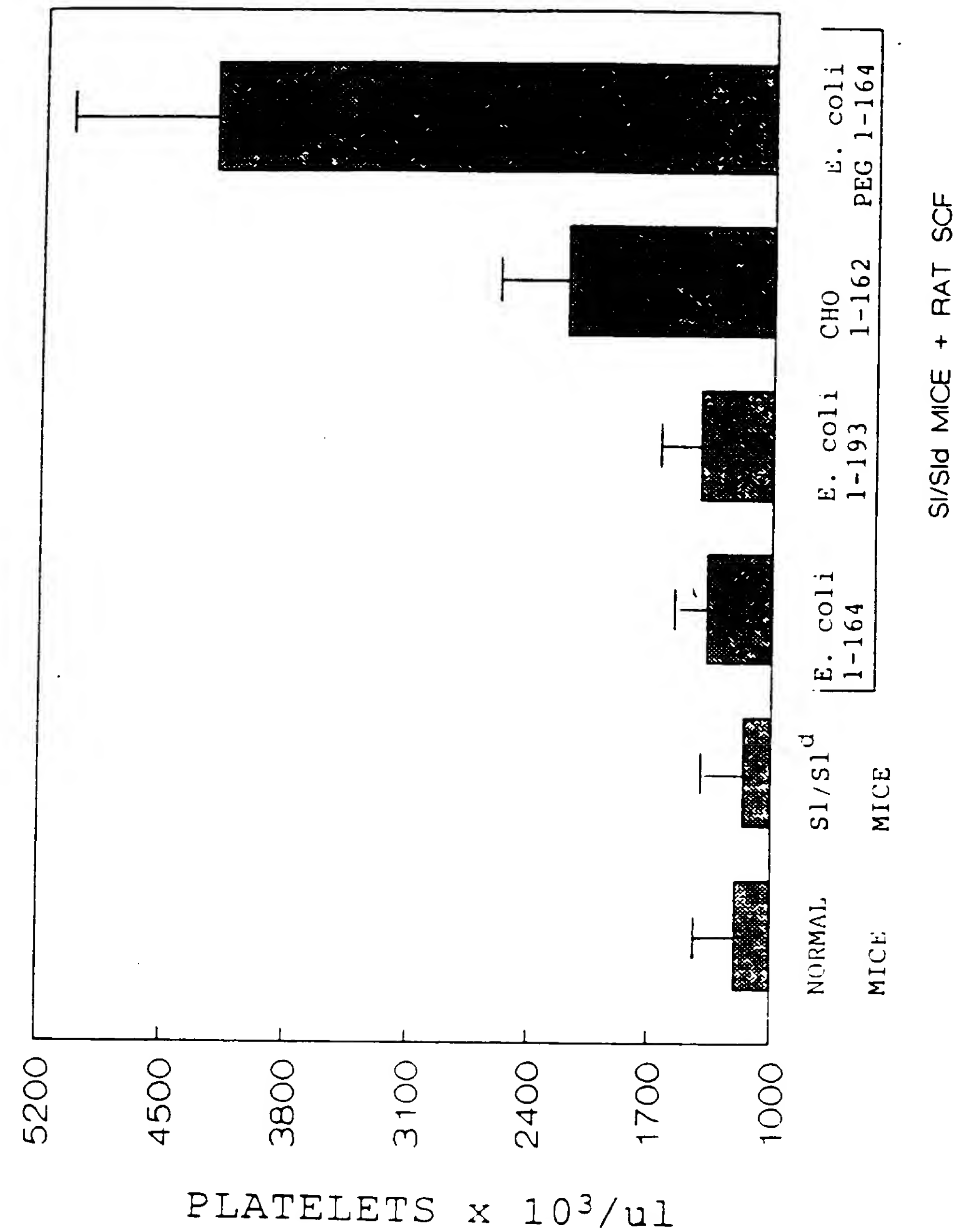
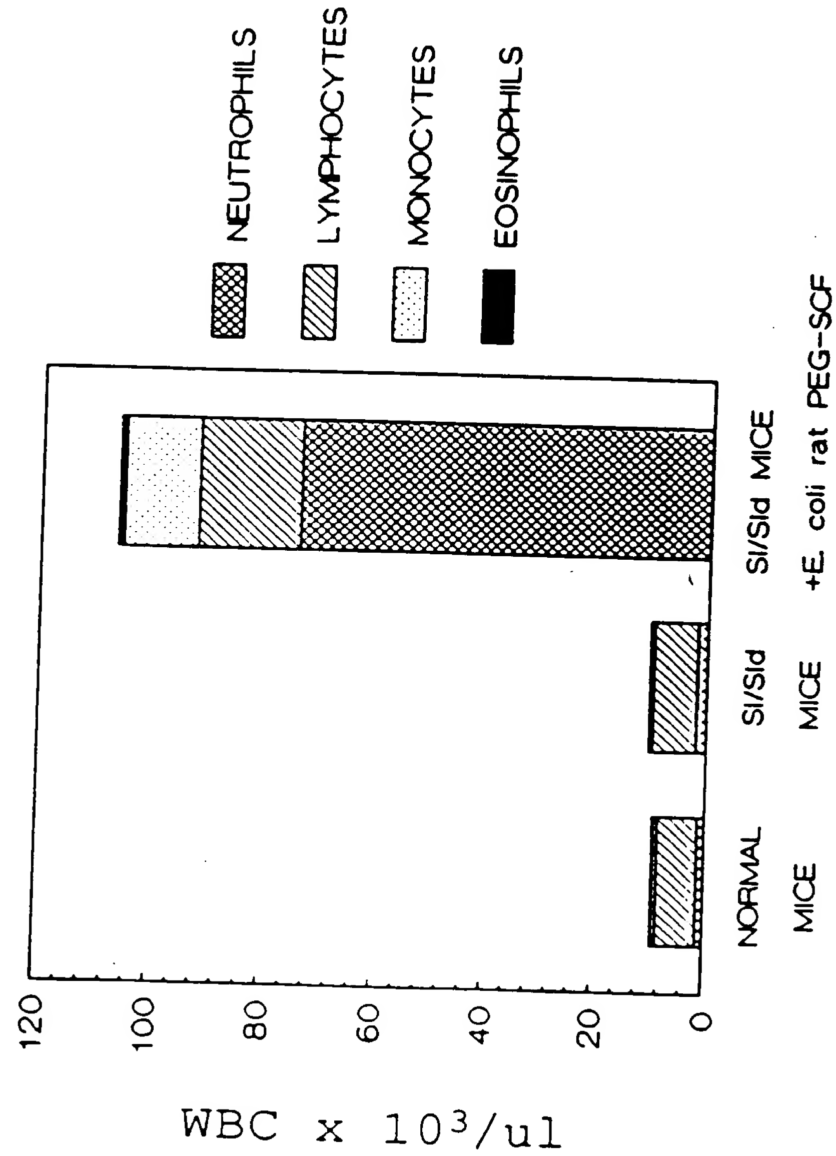
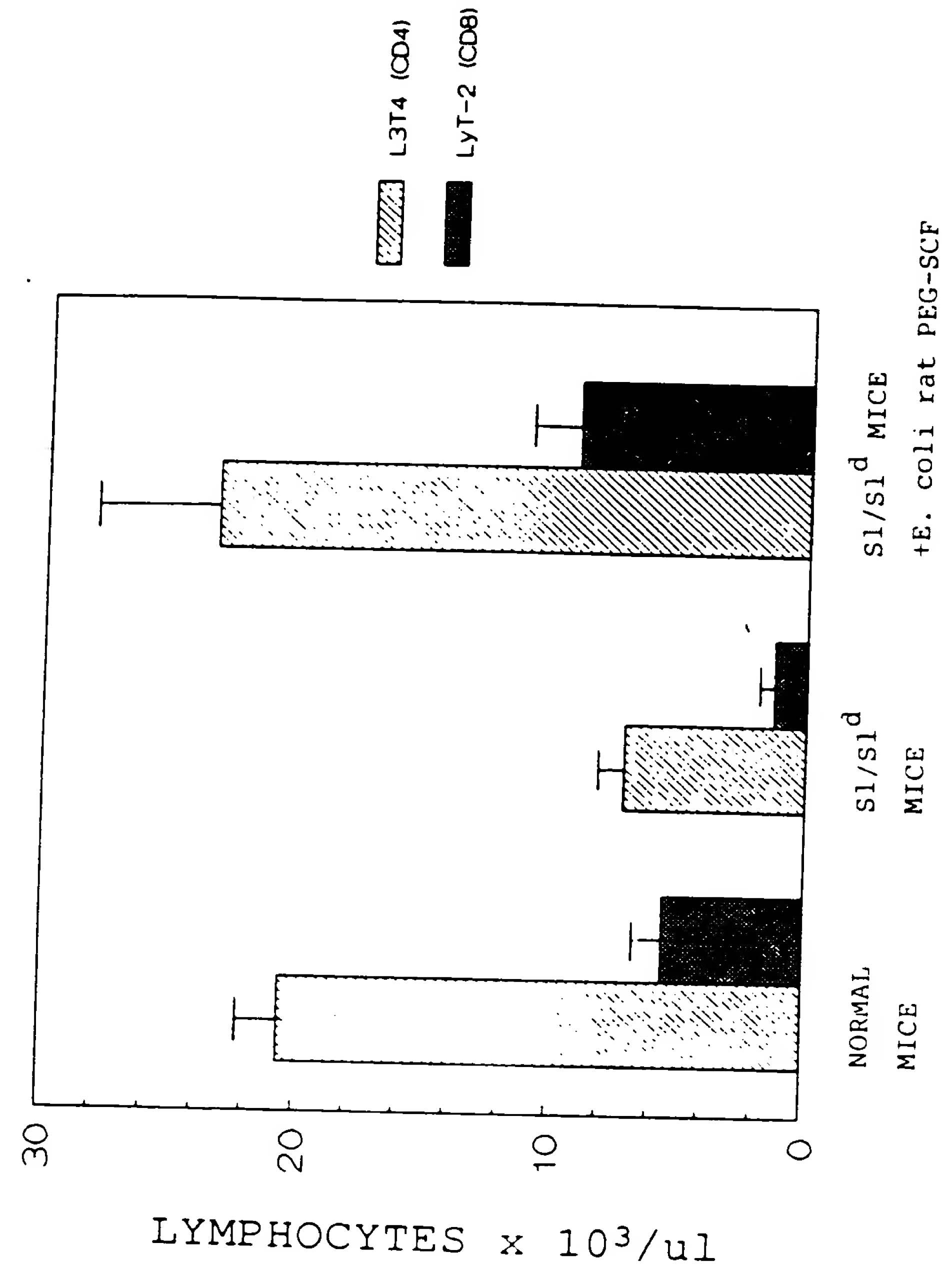

PLATELETS x 10³/ul
5200
4500
3800
3100
2400
1700
1000
NORMAL MICE
Sl/Sl^d MICE
E. coli 1-164
E. coli 1-193
CHO 1-162
E. coli PEG 1-164
Sl/Sld MICE + RAT SCF

FIG.27



NEUTROPHILS
LYMPHOCYTES
MONOCYTES
EOSINOPHILS
WBC x 10³/ul
0
20
40
60
80
100
120
NORMAL MICE
Sl/Sld MICE
Sl/Sld MICE +E. coli rat PEG-SCF

FIG. 28



L3T4 (CD4)
LyT-2 (CD8)
LYMPHOCYTES x 10³/ul
30
20
10
0
NORMAL MICE
Sl/Sl^d MICE
Sl/Sl^d MICE
+E. coli rat PEG-SCF

FIG.29A

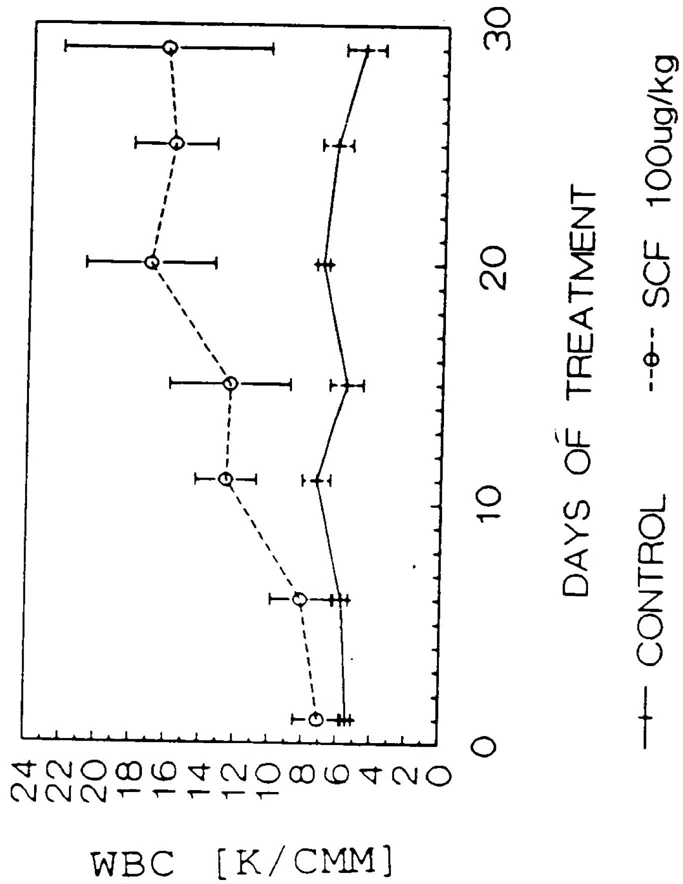

WBC [K/CMM]
0 2 4 6 8 10 12 14 16 18 20 22 24
0 10 20 30
DAYS OF TREATMENT
CONTROL
SCF 100ug/kg

FIG.29B

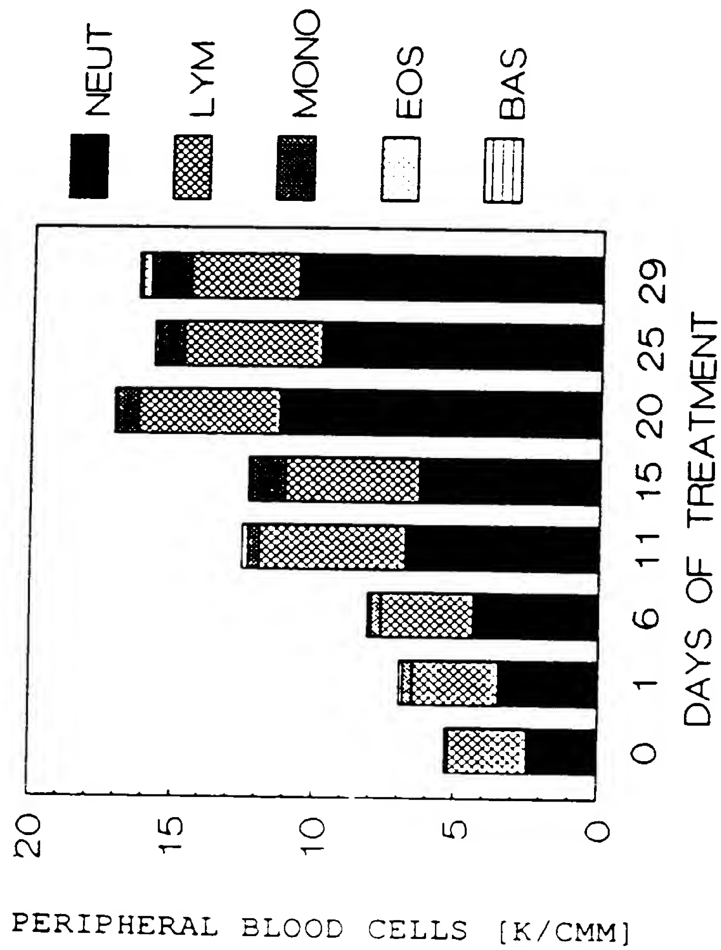

NEUT
LYM
MONO
EOS
BAS
20
15
10
5
0
PERIPHERAL BLOOD CELLS [K/CMM]
0
1
6
11
15
20
25
29
DAYS OF TREATMENT

FIG.30A

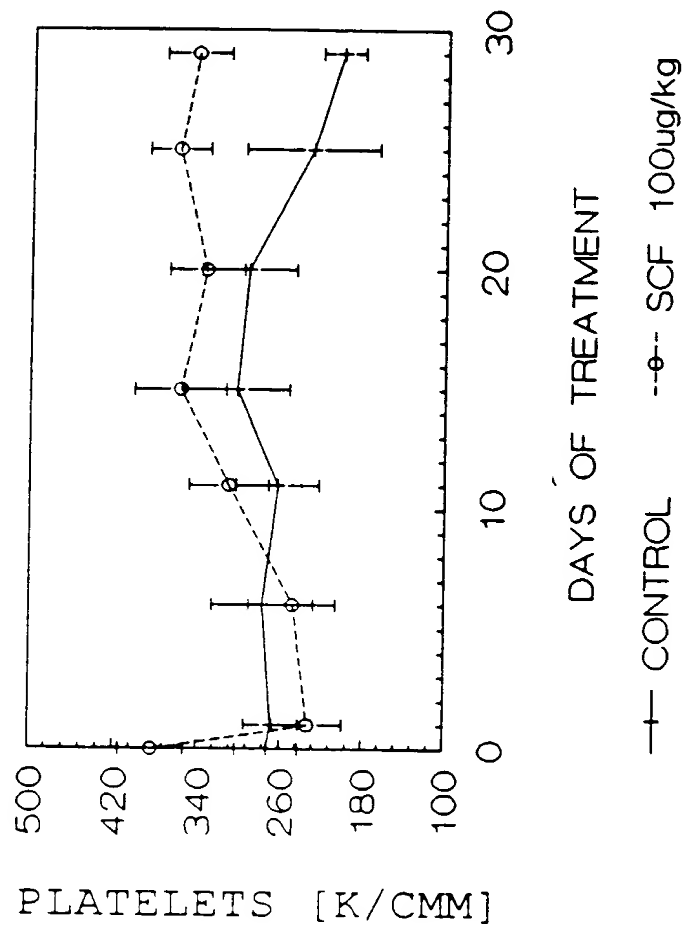

PLATELETS [K/CMM]
500
420
340
260
180
100
0
10
20
30
DAYS OF TREATMENT
CONTROL
SCF 100ug/kg

FIG.30B

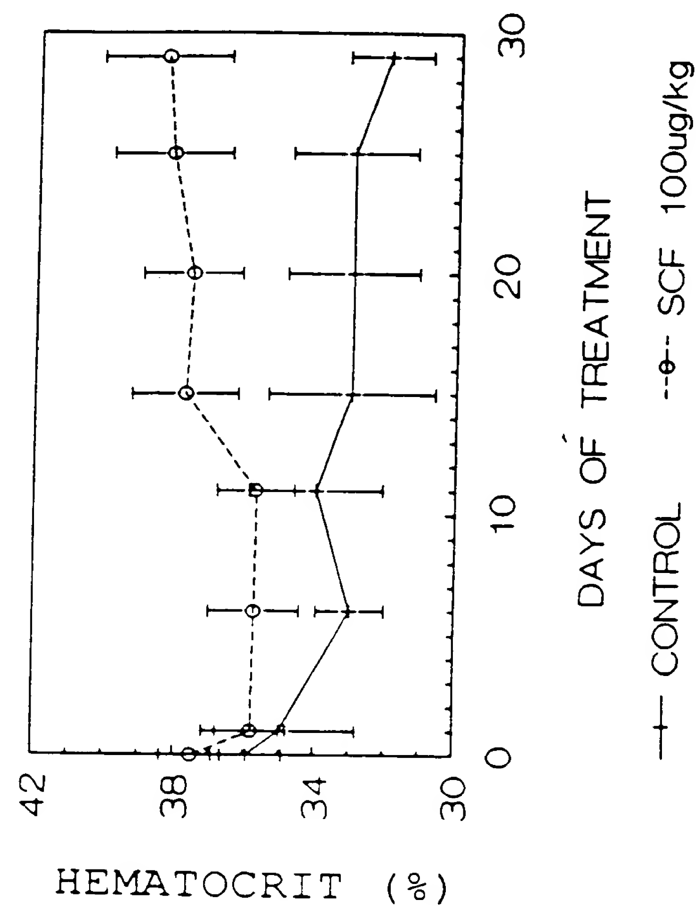

HEMATOCRIT (%)
42
38
34
30
0
10
20
30
DAYS OF TREATMENT
CONTROL
SCF 100ug/kg

FIG. 31A

FIG. 31B

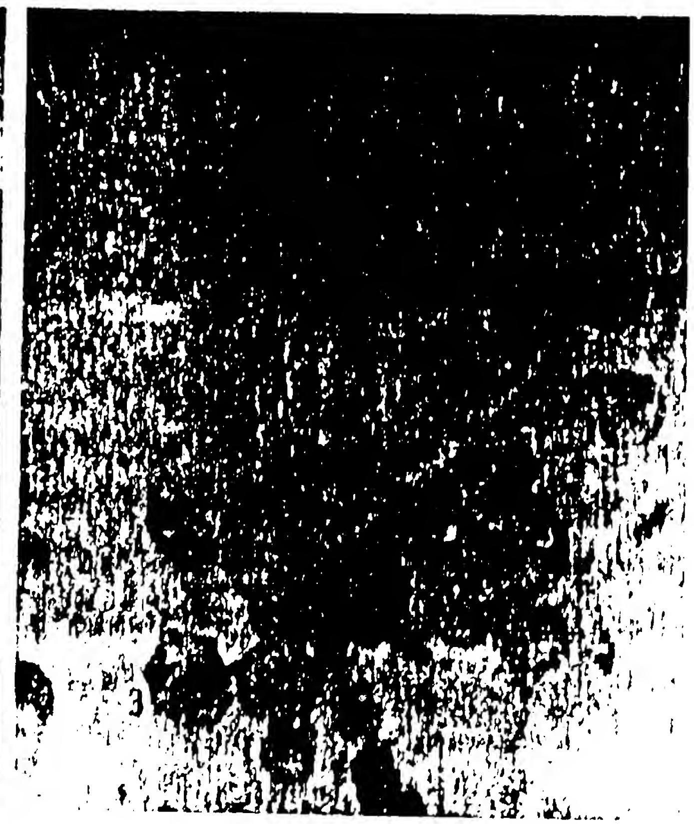


FIG. 31C

SCF4 SMP4

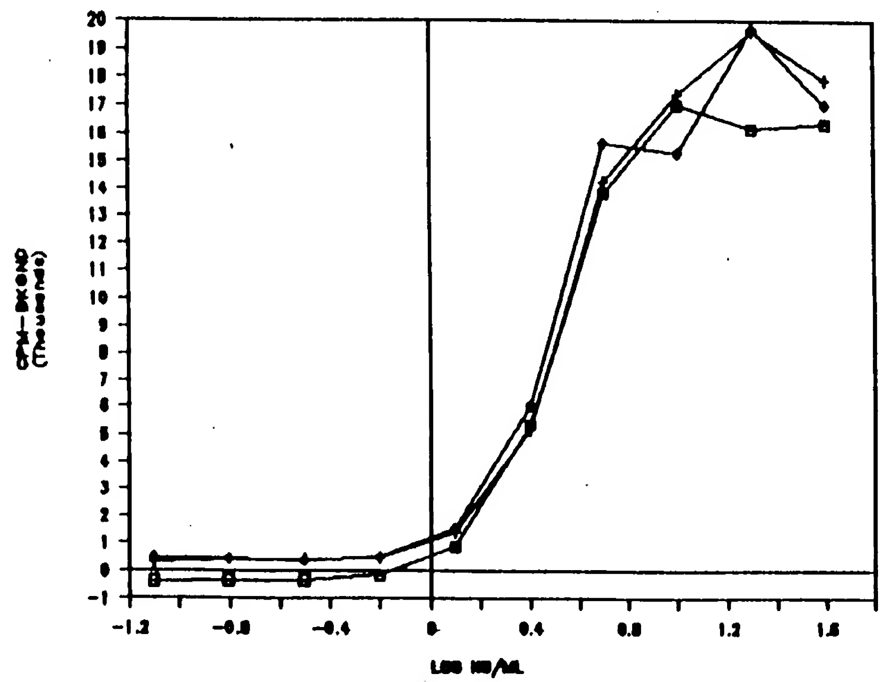


FIG. 32A

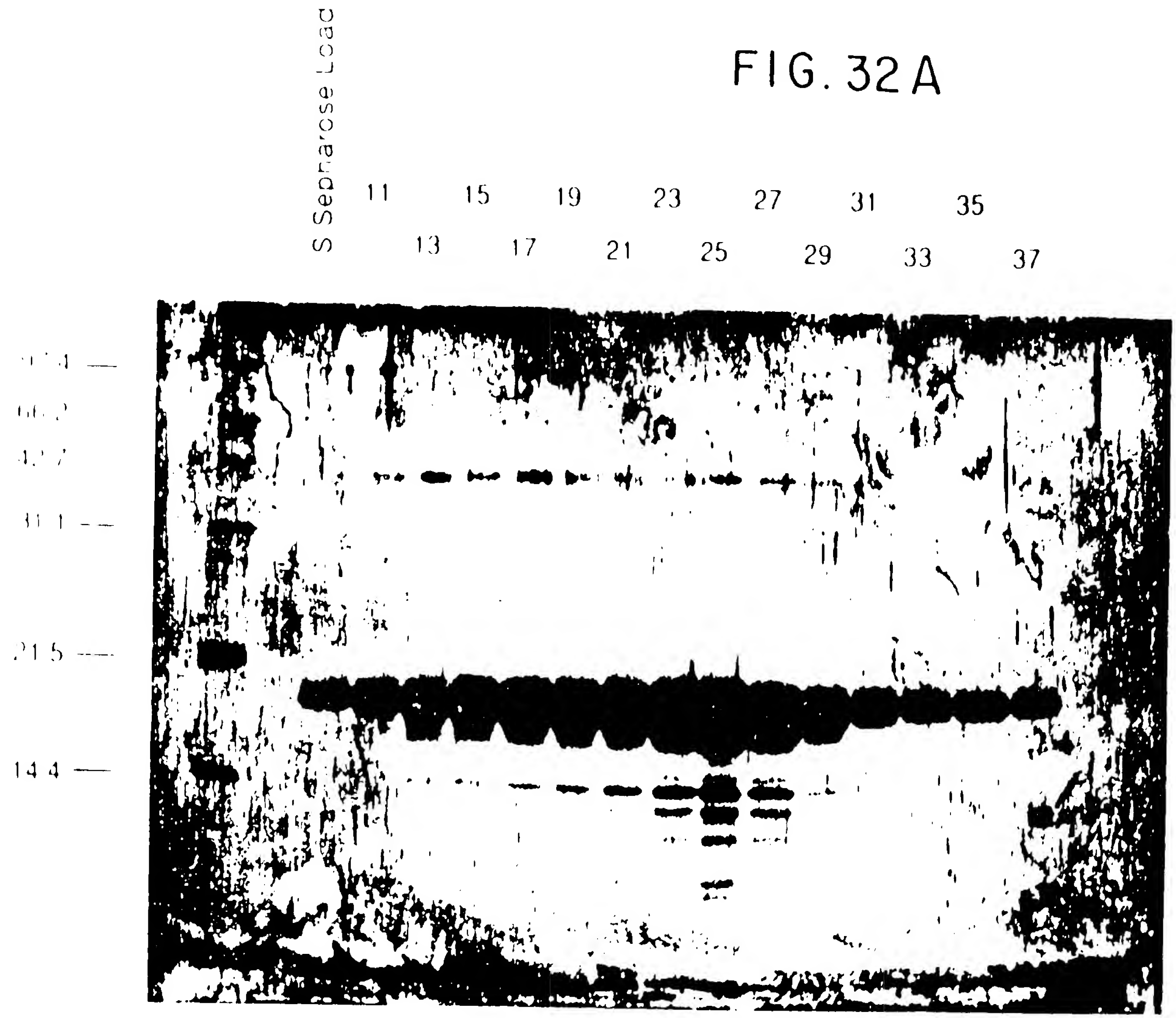
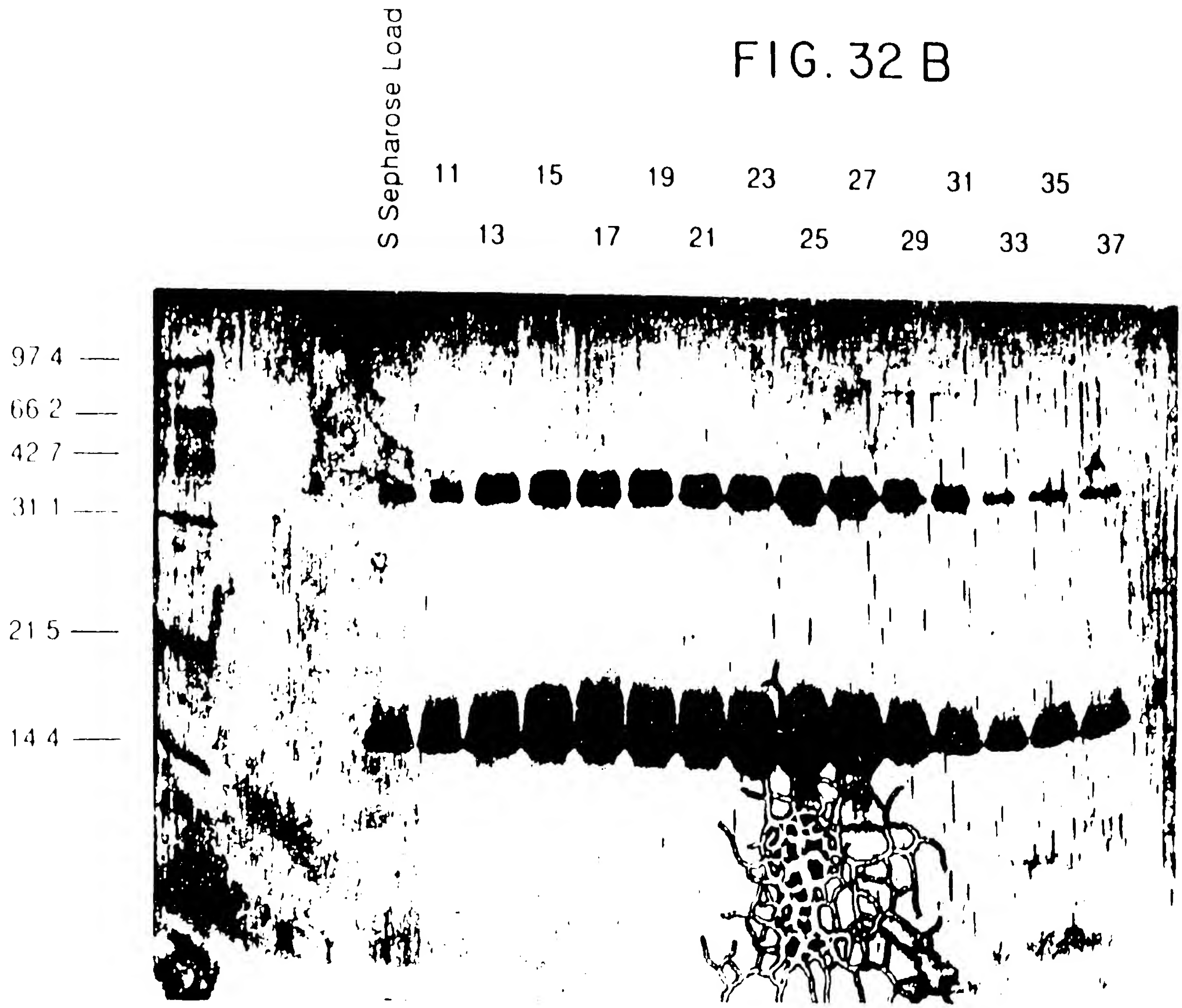


FIG. 32 B



S Sepharose Load
11
13
15
17
19
21
23
25
27
29
31
33
35
37
97 4
66 2
42 7
31 1
21 5
14 4

FIG.33

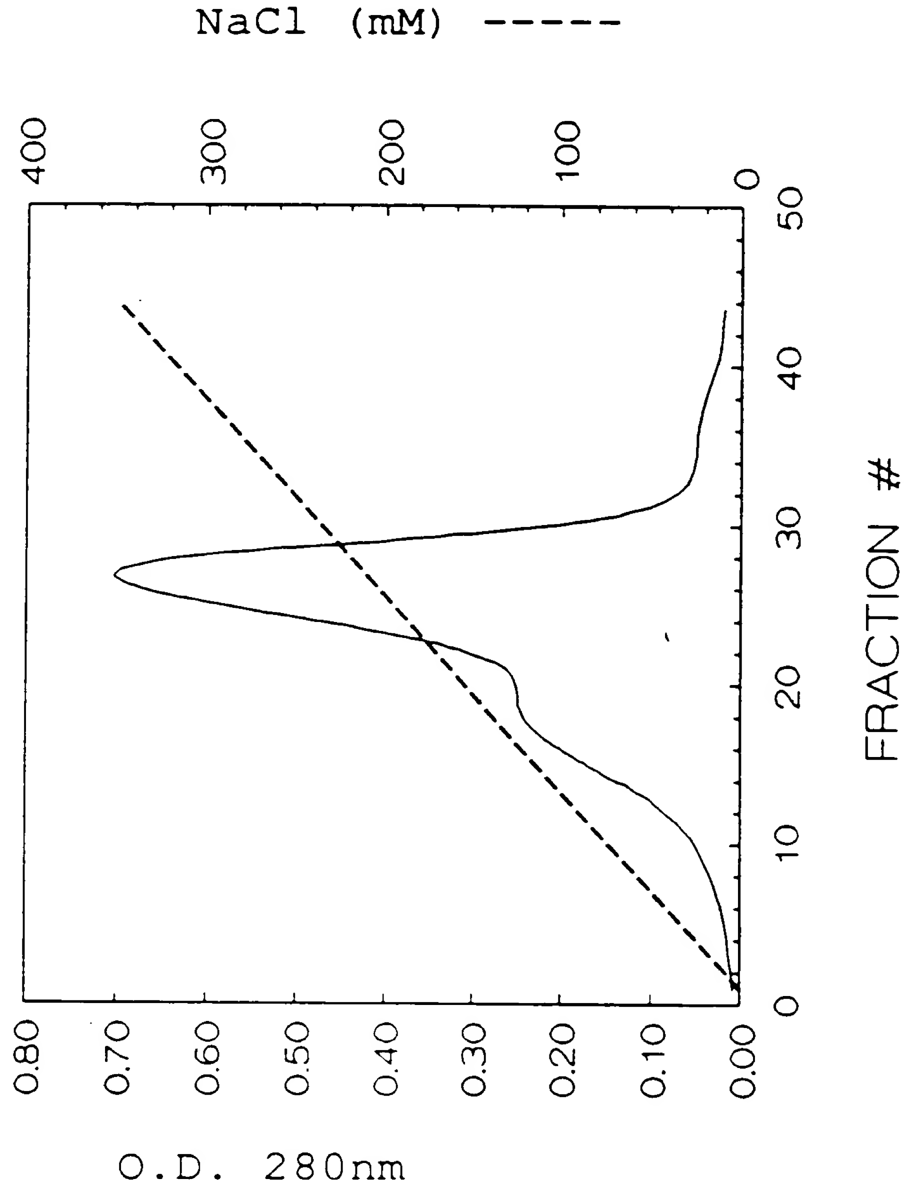

NaCl (mM) -----
400
300
200
100
0
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
0
10
20
30
40
50
FRACTION #
O.D. 280nm ____

FIG.34A

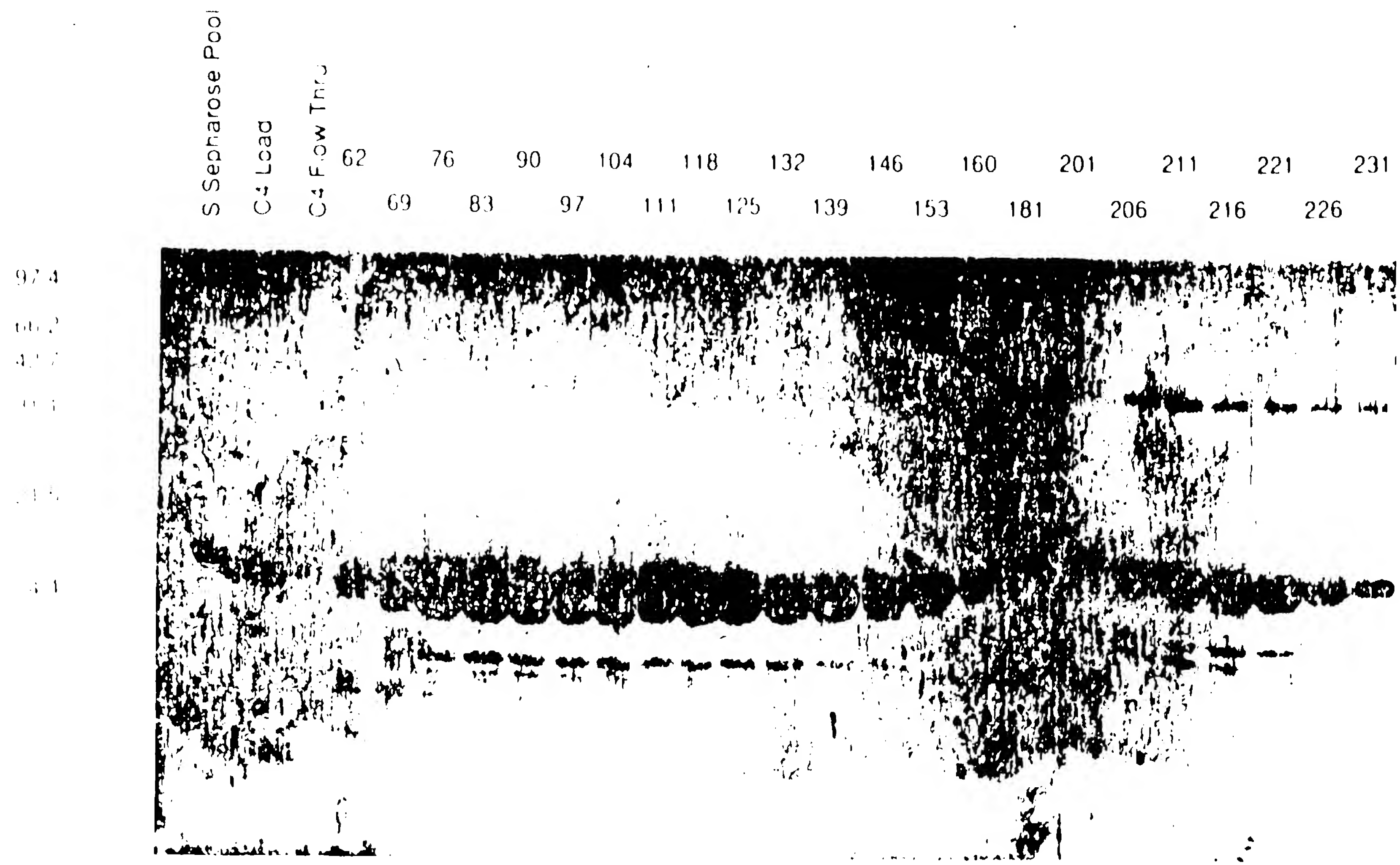
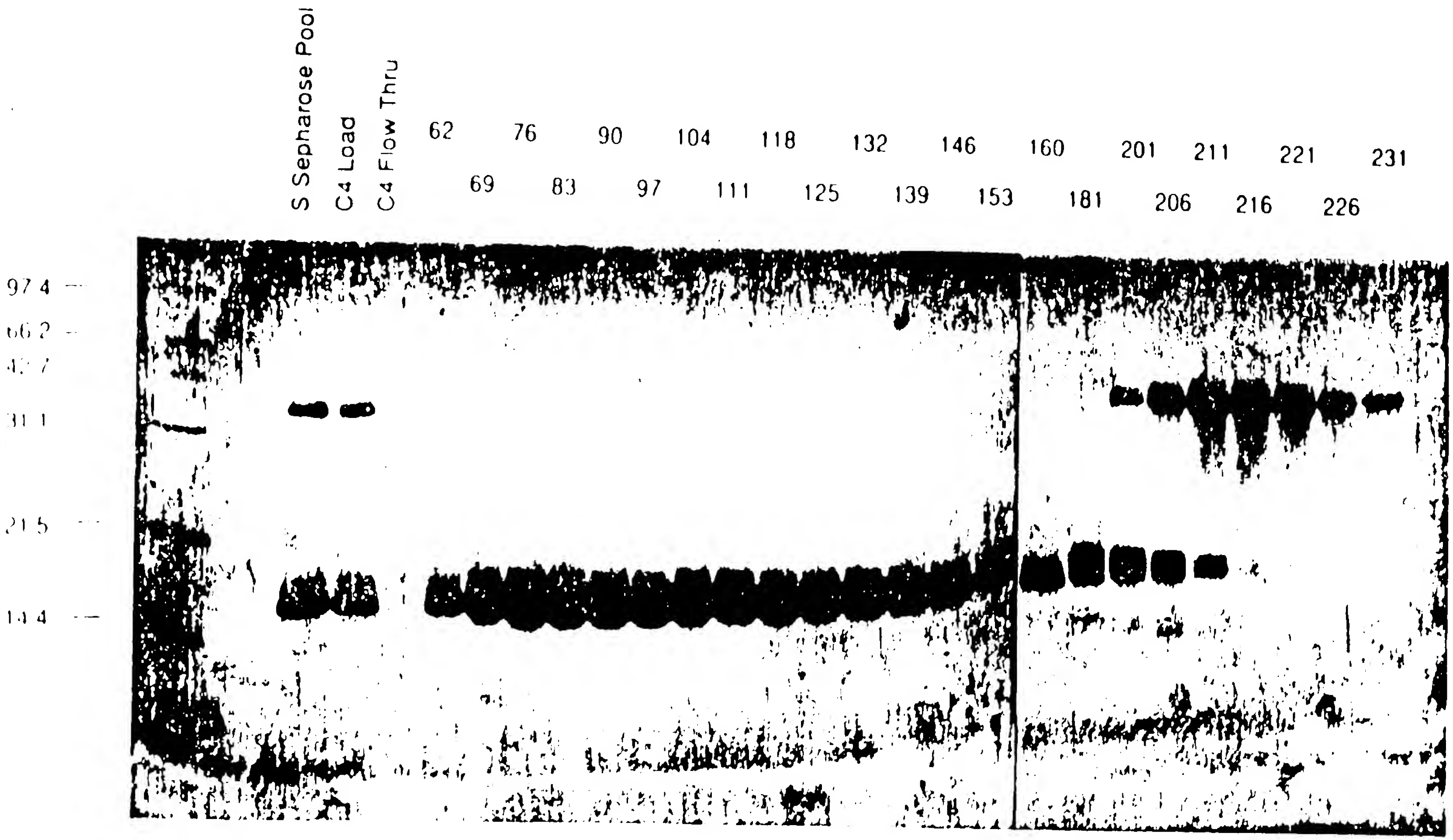
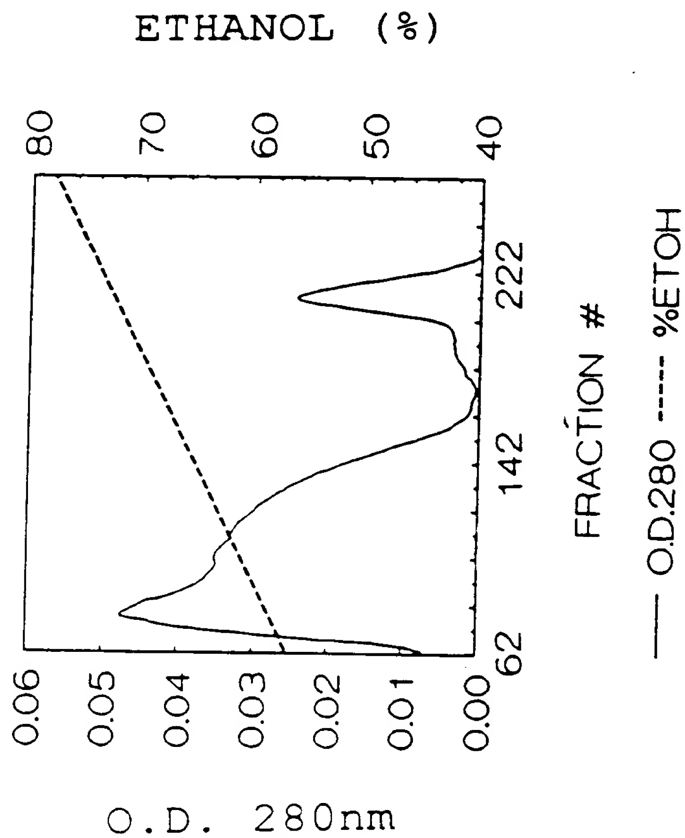

S Sepharose Pool
C4 Load
C4 Flow Thru
62
69
76
83
90
97
104
111
118
125
132
139
146
153
160
181
201
206
211
216
221
226
231
97.4

FIG. 34B



S Sepharose Pool
C4 Load
C4 Flow Thru
62
69
76
83
90
97
104
111
118
125
132
139
146
153
160
181
201
206
211
216
221
226
231
97.4
66.2
31.1
21.5
14.4

FIG. 35



ETHANOL (%)
80
70
60
50
40
0.06
0.05
0.04
0.03
0.02
0.01
0.00
62
142
222
FRACTION #
— O.D.280 ----- %ETOH
O.D. 280nm

FIG. 36

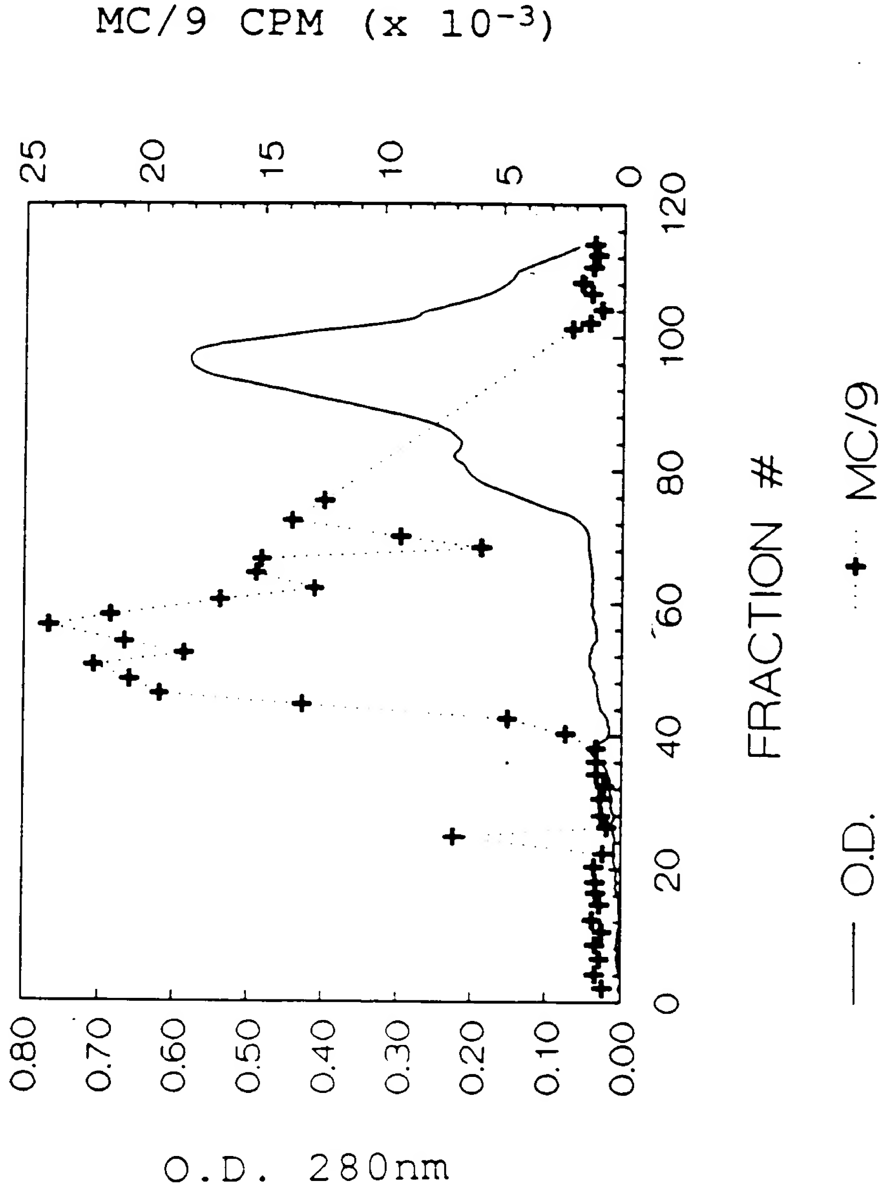
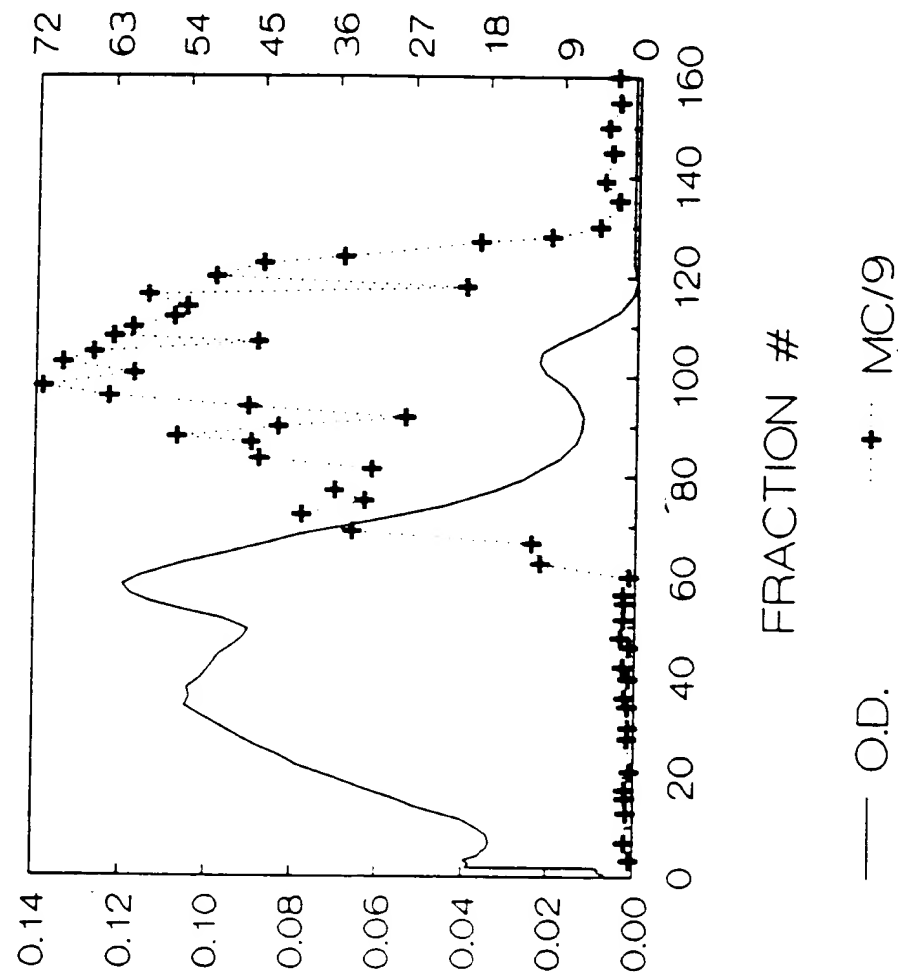


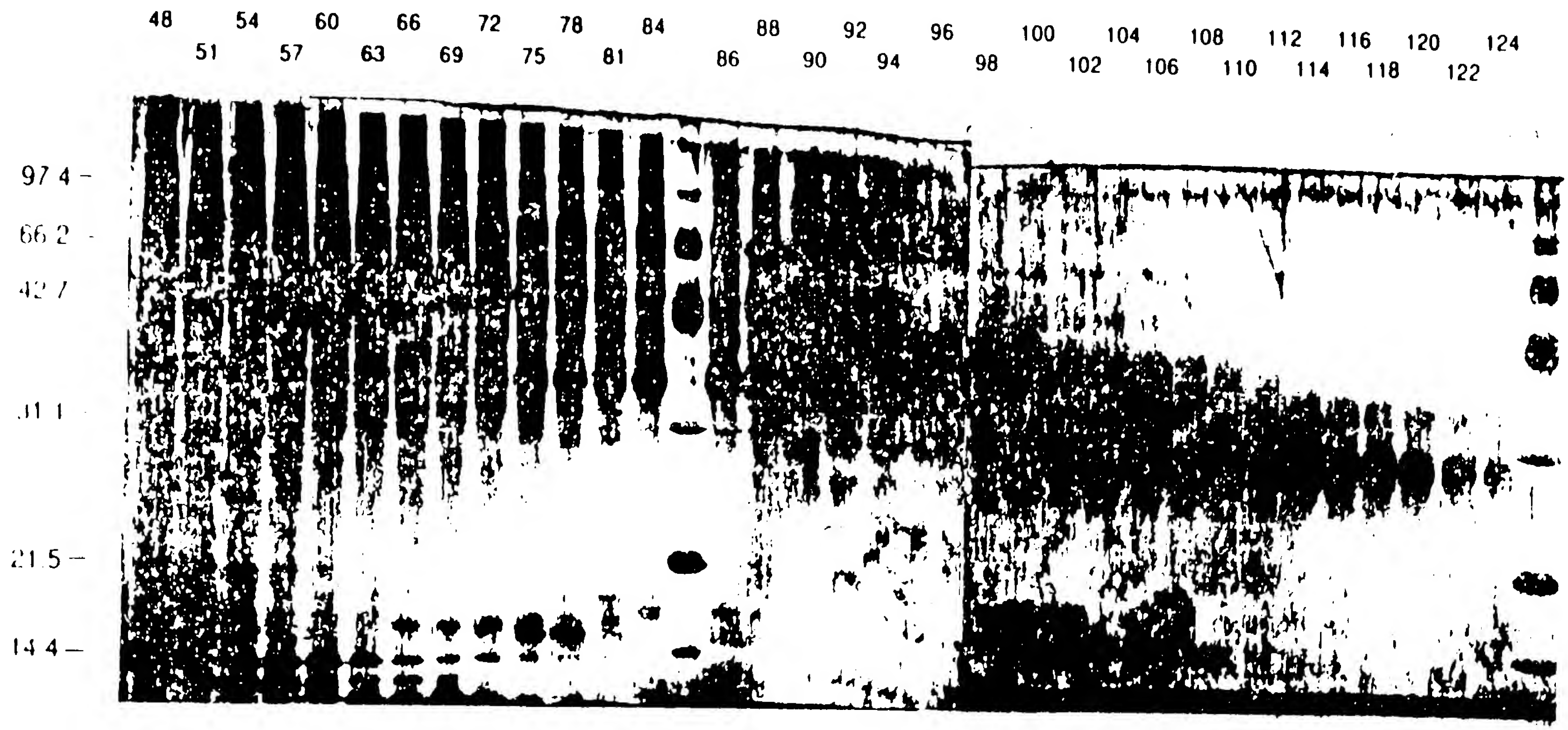
FIG. 37

MC/9 CPM (x 10^{-3})



O.D. 280nm (x 10^{1})

FIG.38



48
51
54
57
60
63
66
69
72
75
78
81
84
86
88
90
92
94
96
98
100
102
104
106
108
110
112
114
116
118
120
122
124
97 4
66 2
42 7
31 1
21 5
14 4

FIG. 39

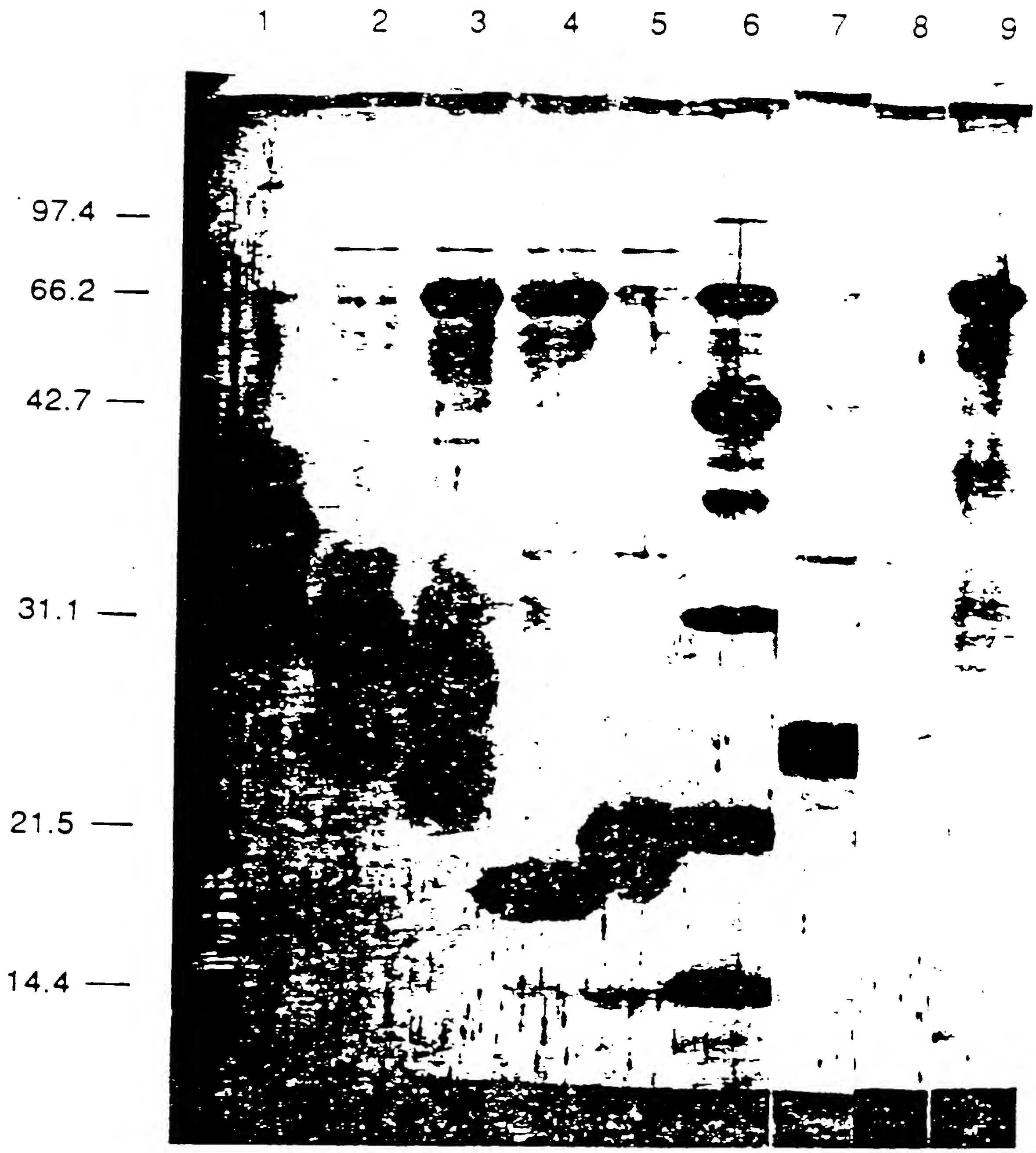


FIG. 40A

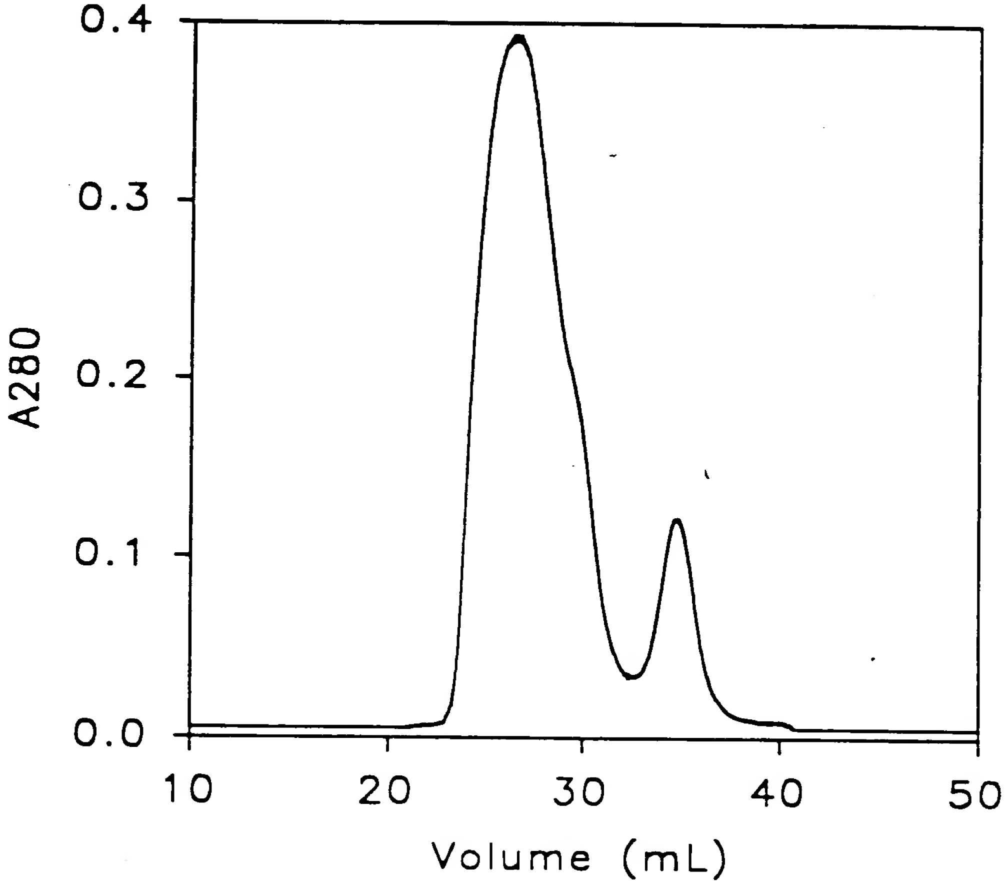


FIG. 40B

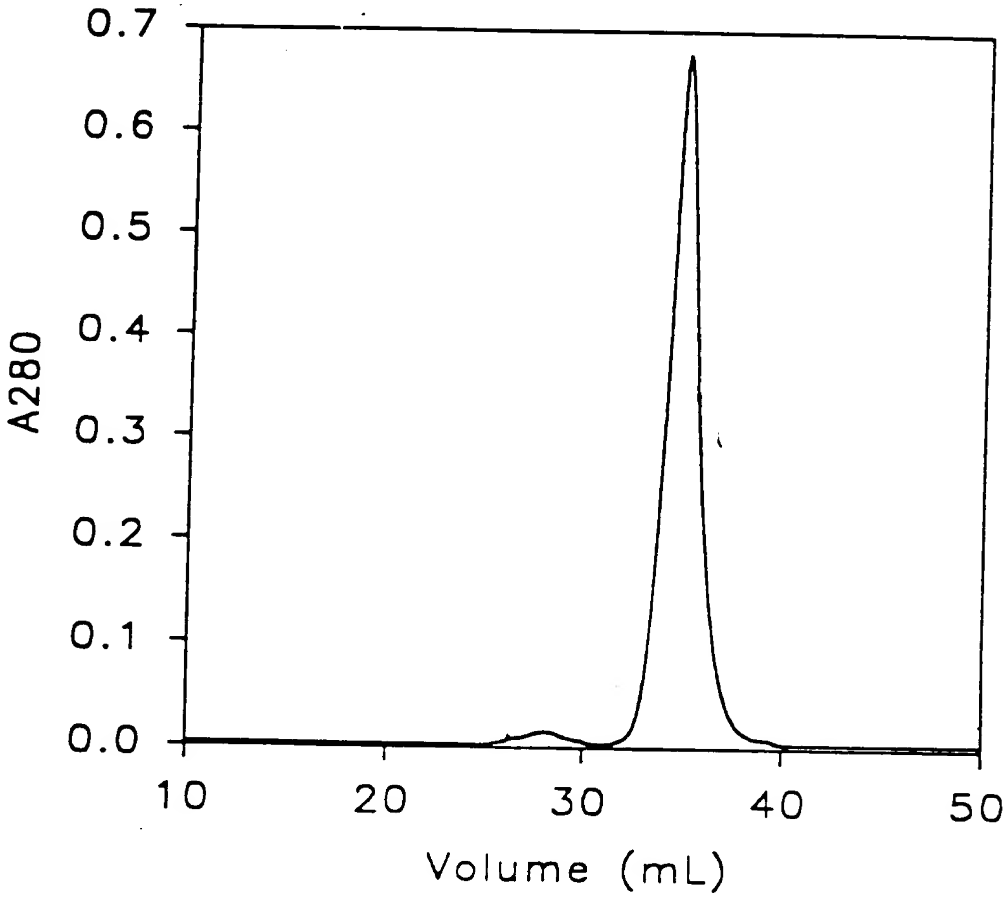


FIG. 41

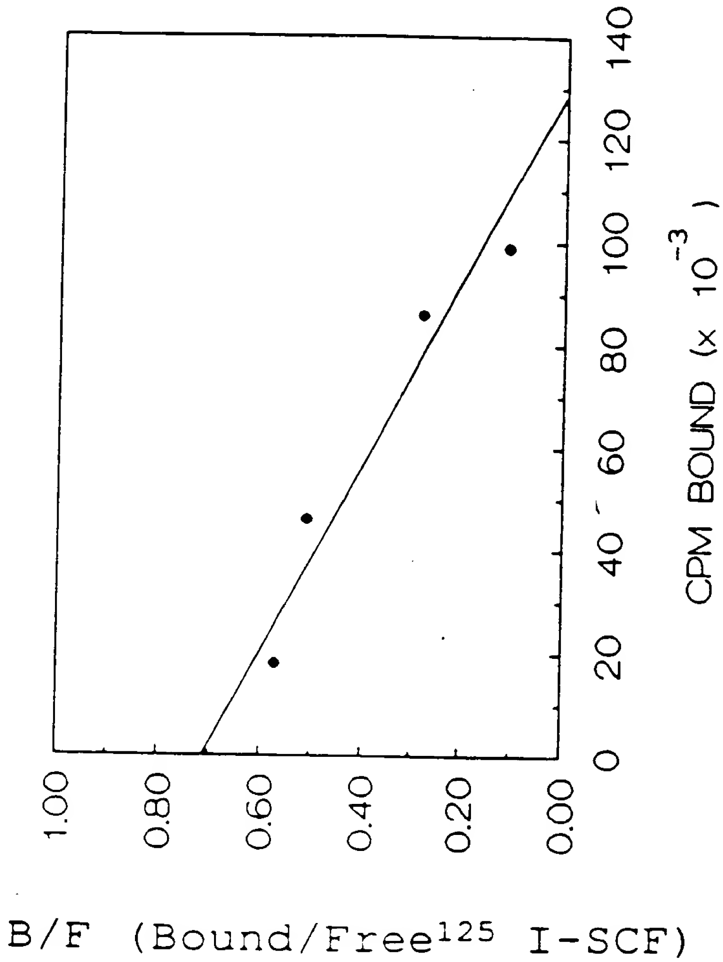

1.00
0.80
0.60
0.40
0.20
0.00
B/F (Bound/Free^{125} I-SCF)
0
20
40
60
80
100
120
140
CPM BOUND (x 10^{-3})

FIG.42A

```
CCGCCTCGCGCCGAGACTAGAAGCGCTGCGGGAAGCAGGGACAGTGGAGAGGGCGCTGCGC  61

TCGGGCTACCCAATGCGTGGACTATCTGCCGCCGCTGTTCGTGCAATATGCTGGAGCTCCA 122

GAACAGCTAAACGGAGTCGCCACACCACTGTTTGTGCTGGATCGCAGCGCTGCCTTTCCTT 183

-25                 -20
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln
ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG    228

-10                                          1
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg
CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG    273

                 10                                      20
Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala
AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA    318

                                     30
Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly
AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG    363

                 40                                      50
Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val
ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA    408

                                     60
Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT    453
```

FIG.42B

```
                    70                                                  80
Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val
ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG    498

                                        90
Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser
AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT    543

                100                                     110
Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe
AAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT    588

                                    120
Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala
ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC    633

                130                                     140
Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val
TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT    678

                                    150
Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg Val Ser Val Thr
TCT TCA ACA TTA AGT CCT GAG AAA GAT TCC AGA GTC AGT GTC ACA    723
```

FIG.42C

```
                    160                                               170
Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu Arg Asn
AAA CCA TTT ATG TTA CCC CCT GTT GCA GCC AGC TCC CTT AGG AAT    768

                                        180
Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro Gly Asp
GAC AGC AGT AGC AGT AAT AGG AAG GCC AAA AAT CCC CCT GGA GAC    813

                    190                                               200
Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe Ser
TCC AGC CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG TTT TCT    858

                                        210
Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg
CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG AAG AGA    903

                    220                                               230
Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu
CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT AAT GAA    948

                                    240
Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe
GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA GAG TTT    993

        248
Gln Glu Val End
CAA GAA GTG TAA      TTGTGGCTTGTATCAACACTGTTACTTTCGTACATTGGC 1044
```

FIG.42D

TGGTAACAGTTCATGTTTGCTTCATAAATGAAGCAGCTTTAAACAAATTCATATTCTGTC 1104

TGGAGTGACAGACCACATCTTTATCTGTTCTTGCTACCCATGACTTTATATGGATGATTC 1164

AGAAATTGGAACAGAATGTTTTACTGTGAAACTGGCACTGAATTAATCATCTATAAAGAA 1224

GAACTTGCATGGAGCAGGACTCTATTTTAAGGACTGCGGGACTTGGGTCTCATTTAGAAC 1284

TTGCAGCTGATGTTGGAAGAGAAAGCACGTGTCTCAGACTGCATGTACCATTTGCATGGC 1344

TCCAGAAATGTCTAAATGCTGAAAAAACACCTAGCTTTATTCTTCAGATACAAACTGCAG 1404

FIG. 43

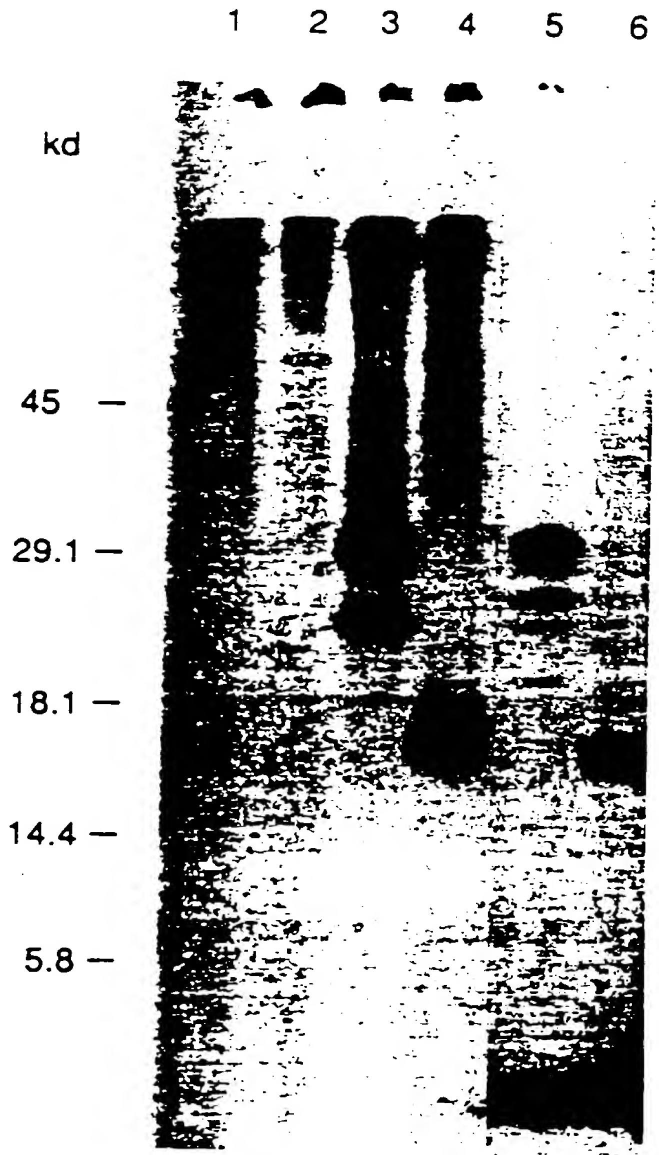


FIG. 44A

```
                              AGCAGGGACAGTGGAGAGGGCGCTGCGCTC  30

GGGCTACCCAATGCGTGGACTATCTGCCGCCGCTGTTCGTGCAATATGCTGGAGCTCCAG  90

AACAGCTAAACGGAGTCGCCACACCACTGTTTGTGCTGGATCGCAGCGCTGCCTTTCCTT  150

-25                 -20
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln
ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG  195

-10                                         1
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg
CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG  240

                10                                      20
Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala
AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA  285

                                    30
Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly
AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG  330

                40                                      50
Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val
ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA  375
```

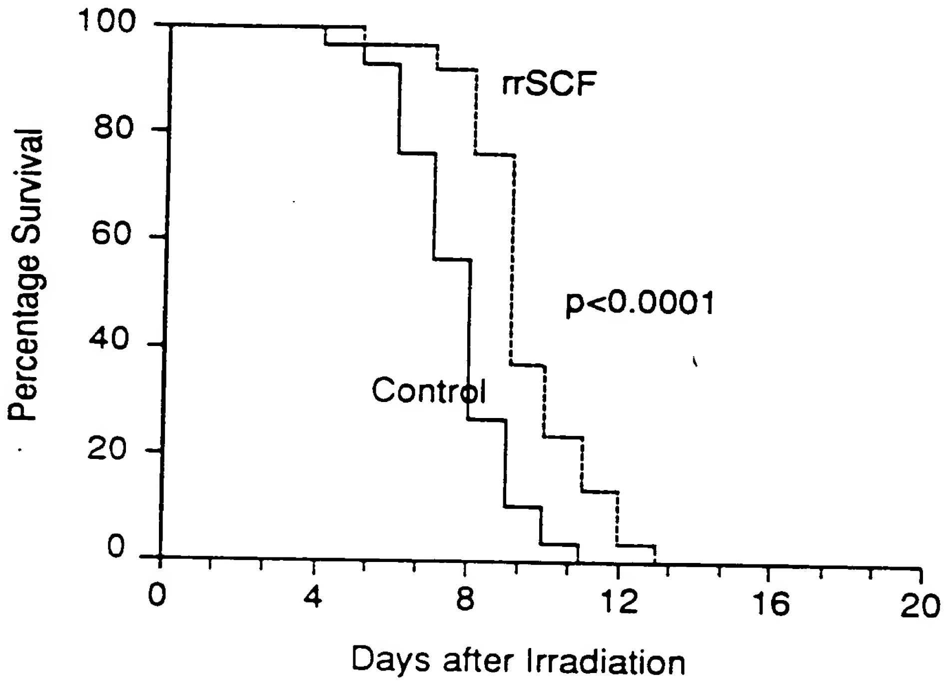
FIG.44B

```
                                             60
Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT    420

                70                                         80
Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val
ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG    465

                                     90
Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser
AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT    510

                100                                       110
Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe
AAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT    555

                                    120
Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala
ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC    600

                130                                       140
Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val
TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT    645

                                       150
Ser Ser Thr Leu Ser Pro Glu Lys | Gly | Lys Ala Lys Asn Pro Pro
TCT TCA ACA TTA AGT CCT GAG AAA | GGG | AAG GCC AAA AAT CCC CCT    690
```

FIG. 44C

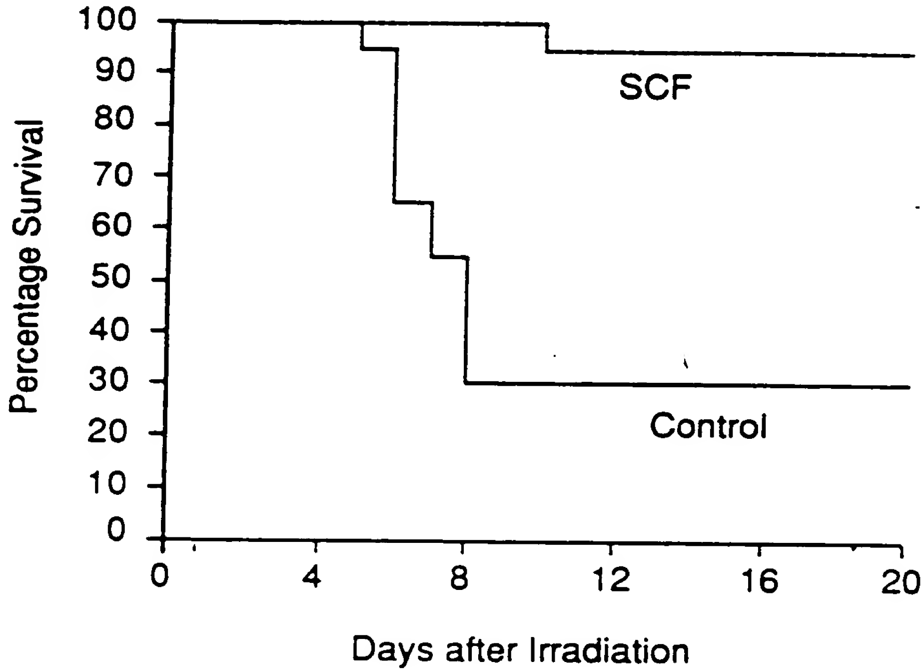
```
                    160                                                 170
Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu
GGA GAC TCC AGC CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG     735

                                        180
Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys
TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG     780

                    190                                         200
Lys Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile
AAG AGA CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT     825

                                        210
Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg
AAT GAA GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA     870

                    220
Glu Phe Gln Glu Val End
GAG TTT CAA GAA GTG TAA    TTGTGGCTTGTATCAACACTGTTACTTTCGTA     920

CATTGGCTGGTAACAGTTCATGTTTGCTTCATAAATGAAGCAGCTTTAAACAAATTCATA     980

TTCTGTCTGGAGTGACAGACCACATCTTTATCTGTTCTTGCTACCCATGACTTTATATGG    1040

ATGATTCAGAAATTGGAACAGAATGTTTTACTGTGAAACTGGCACTGA                1088
```

FIG. 45



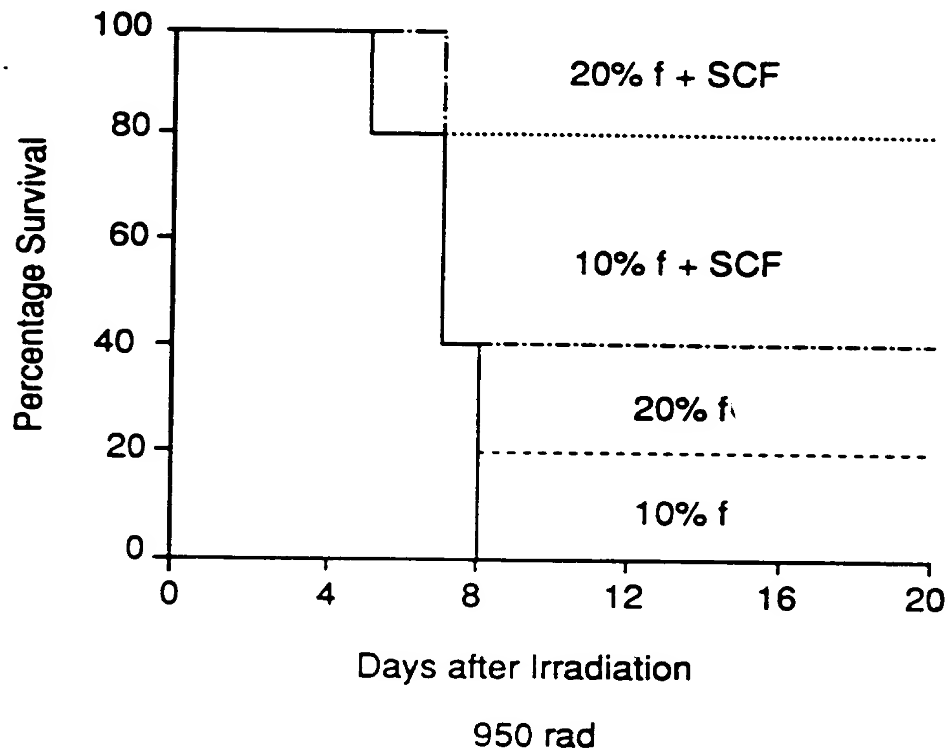
100
80
60
40
20
0
Percentage Survival
rrSCF
p<0.0001
Control
0
4
8
12
16
20
Days after Irradiation

FIG. 46



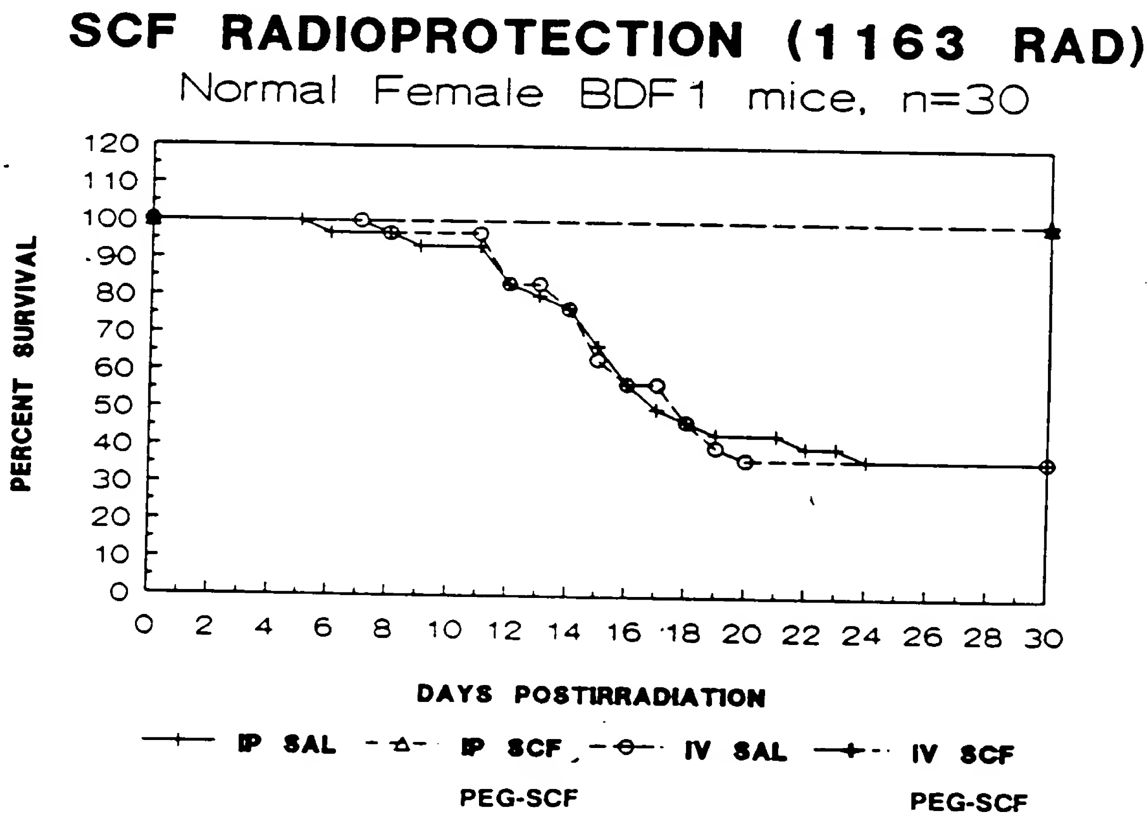
850 RADS; 5% of femur transplanted

FIG. 47



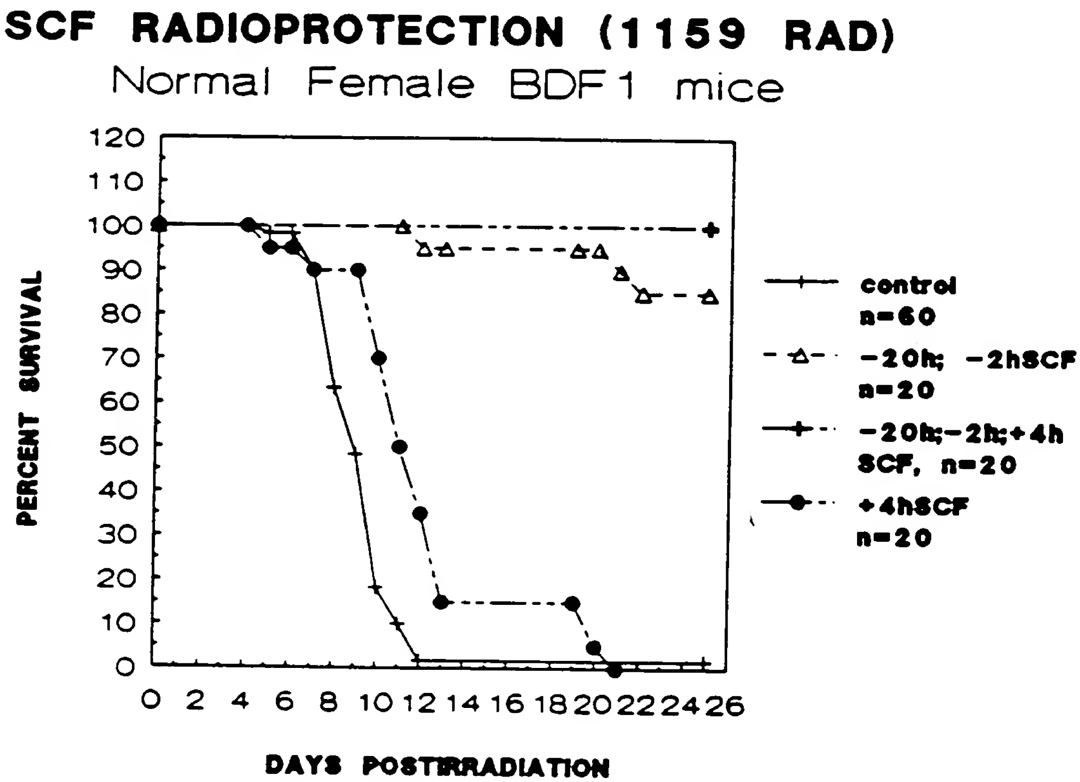
100
80
60
40
20
0
Percentage Survival
20% f + SCF
10% f + SCF
20% f
10% f
0
4
8
12
16
20
Days after Irradiation
950 rad

FIG. 48



SCF RADIOPROTECTION (1163 RAD)
Normal Female BDF1 mice, n=30
PERCENT SURVIVAL
120
110
100
90
80
70
60
50
40
30
20
10
0
0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30
DAYS POSTIRRADIATION
IP SAL
IP SCF PEG-SCF
IV SAL
IV SCF PEG-SCF

FIG. 49



SCF RADIOPROTECTION (1159 RAD)
Normal Female BDF1 mice
PERCENT SURVIVAL
120
110
100
90
80
70
60
50
40
30
20
10
0
0 2 4 6 8 10 12 14 16 18 20 22 24 26
DAYS POSTIRRADIATION
control
n=60
-20h; -2hSCF
n=20
-20h;-2h;+4h
SCF, n=20
+4hSCF
n=20

FIG. 50

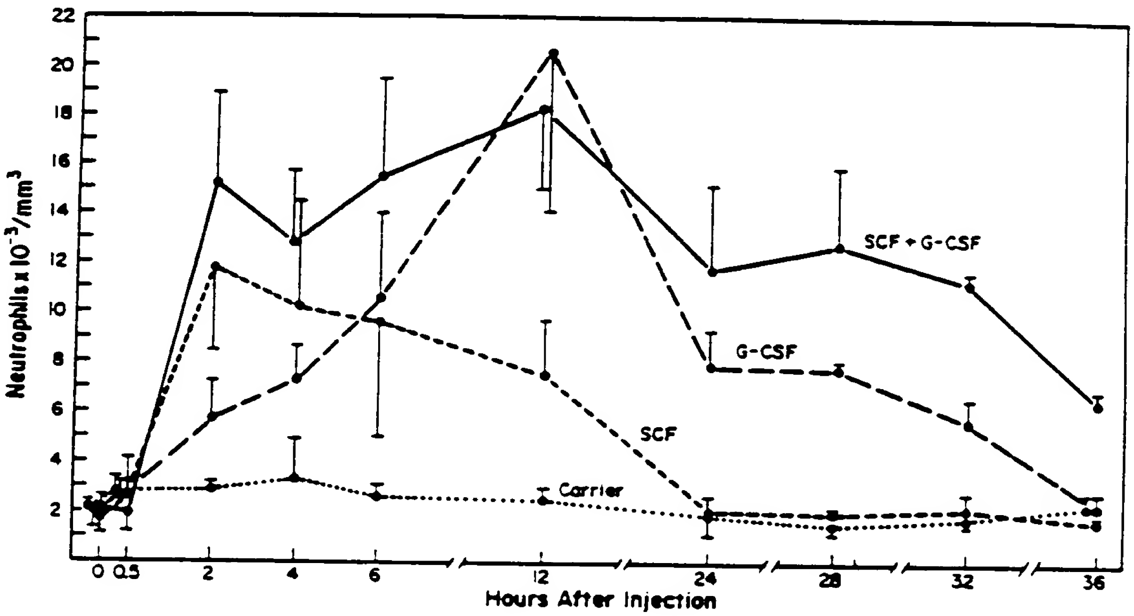
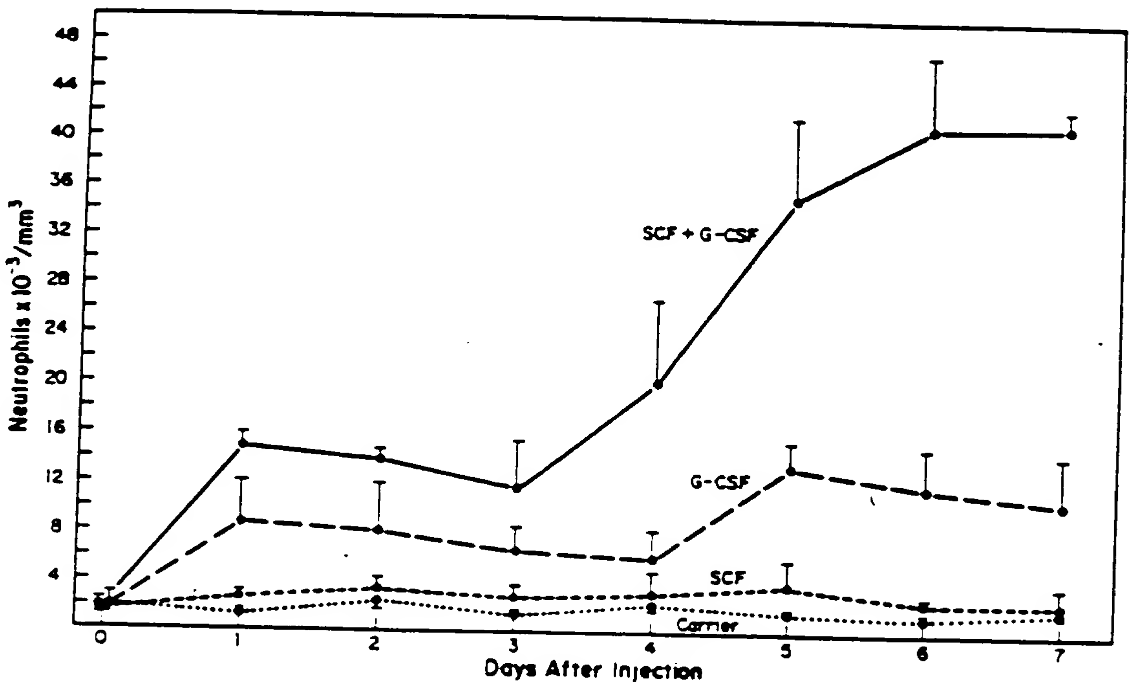
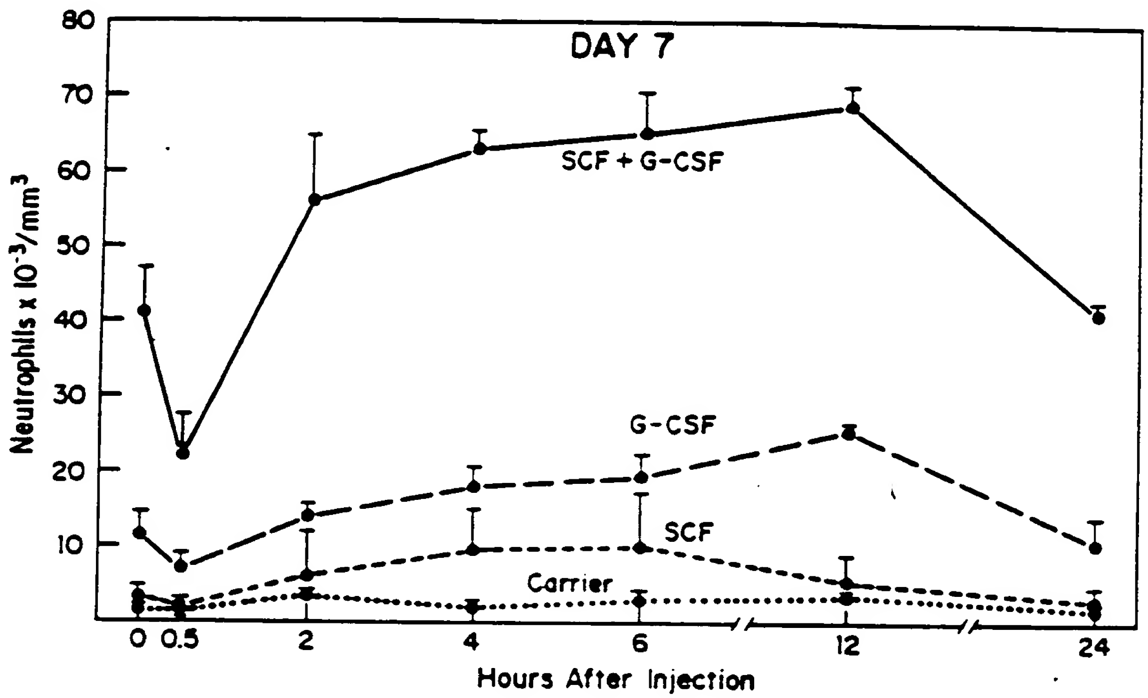

22
20
18
16
14
12
10
8
6
4
2
Neutrophils x 10^{-3}/mm^3
0
0.5
2
4
6
12
24
28
32
36
Hours After Injection
SCF + G-CSF
G-CSF
SCF
Carrier

FIG. 51



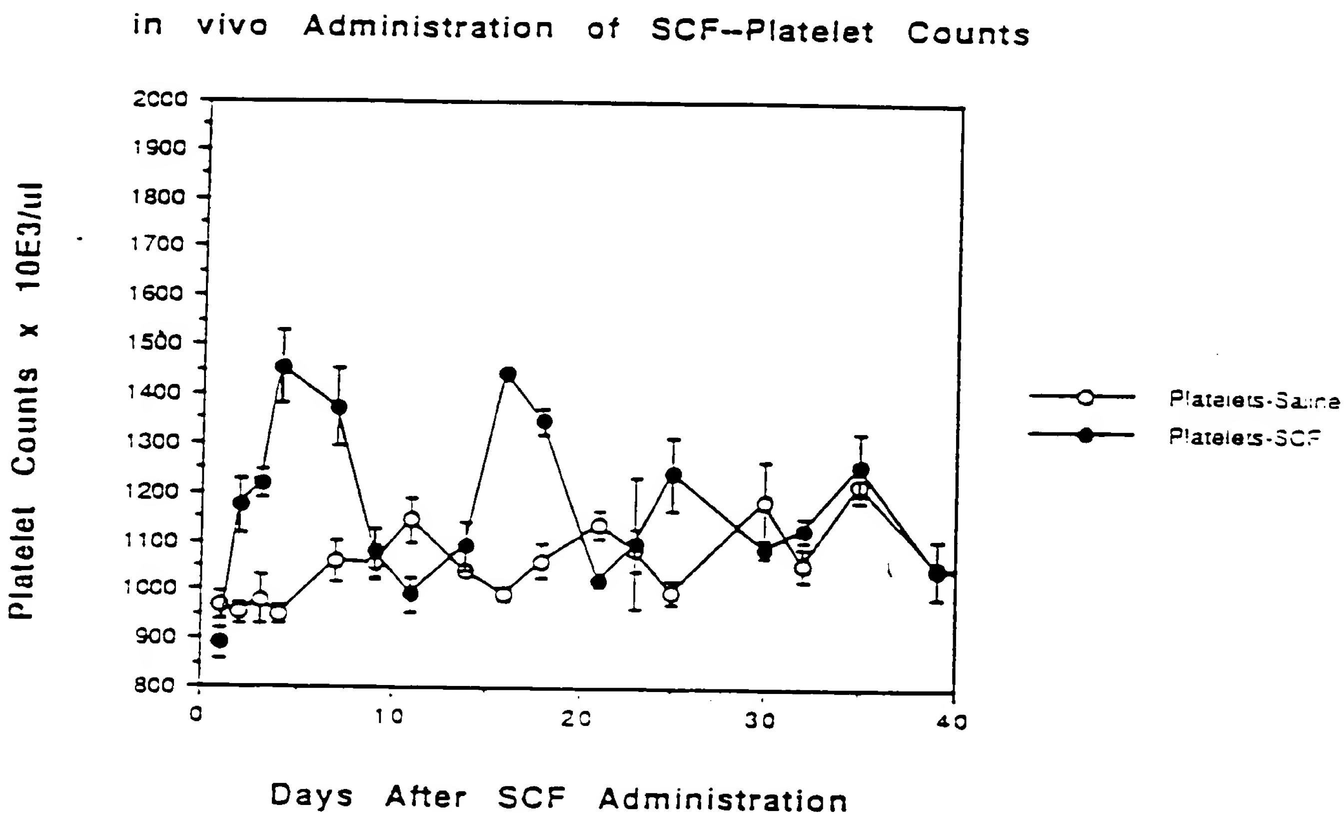
48
44
40
36
32
28
24
20
16
12
8
4
Neutrophils x 10^{-3}/mm^3
SCF + G-CSF
G-CSF
SCF
Carrier
0
1
2
3
4
5
6
7
Days After Injection

FIG. 52



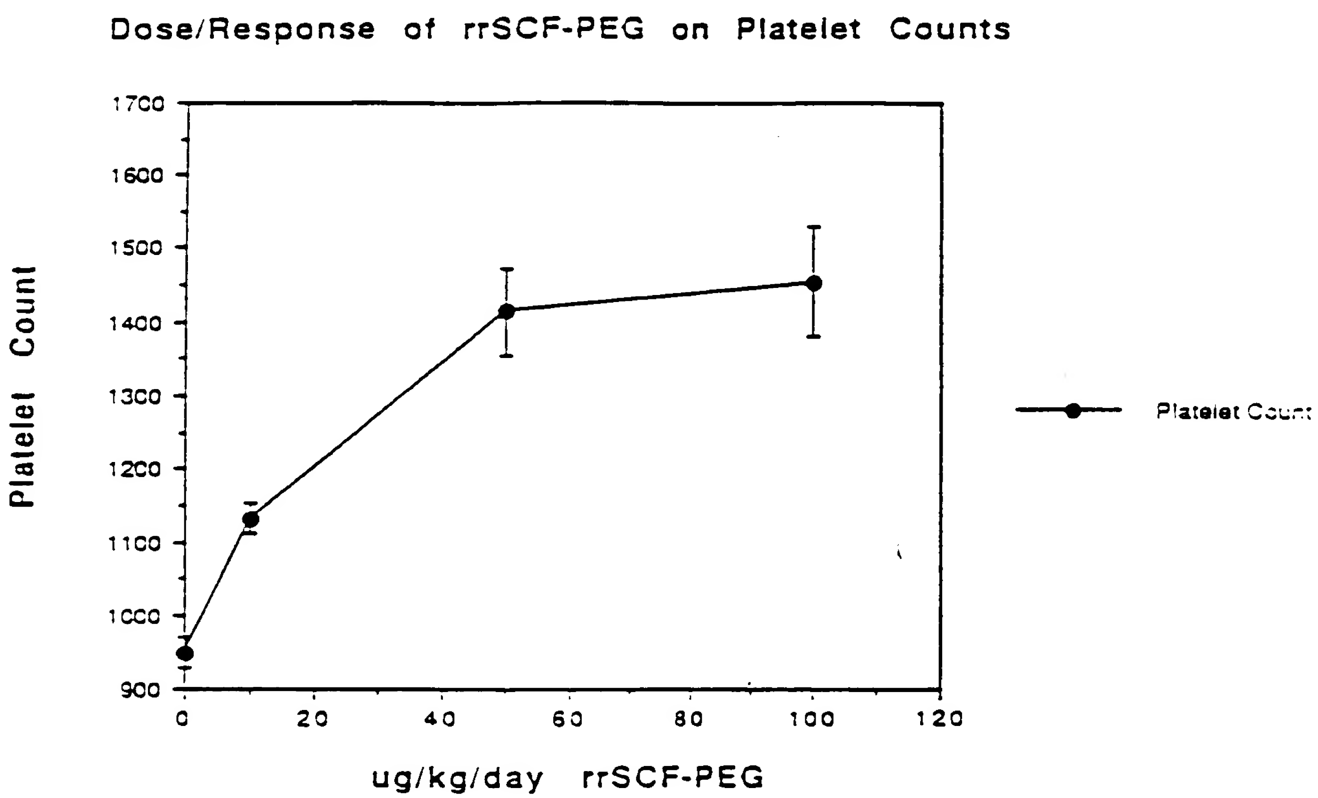
DAY 7
SCF + G-CSF
G-CSF
SCF
Carrier
Neutrophils x 10^{-3}/mm^3
80
70
60
50
40
30
20
10
0
0.5
2
4
6
12
24
Hours After Injection

FIG. 53



in vivo Administration of SCF--Platelet Counts
2000
1900
1800
1700
1600
1500
1400
1300
1200
1100
1000
900
800
0
10
20
30
40
Platelet Counts x 10E3/ul
Days After SCF Administration
Platelets-Saline
Platelets-SCF

FIG. 54



Dose/Response of rrSCF-PEG on Platelet Counts
Platelet Count
1700
1600
1500
1400
1300
1200
1100
1000
900
0
20
40
60
80
100
120
ug/kg/day rrSCF-PEG
Platelet Count

FIG. 55

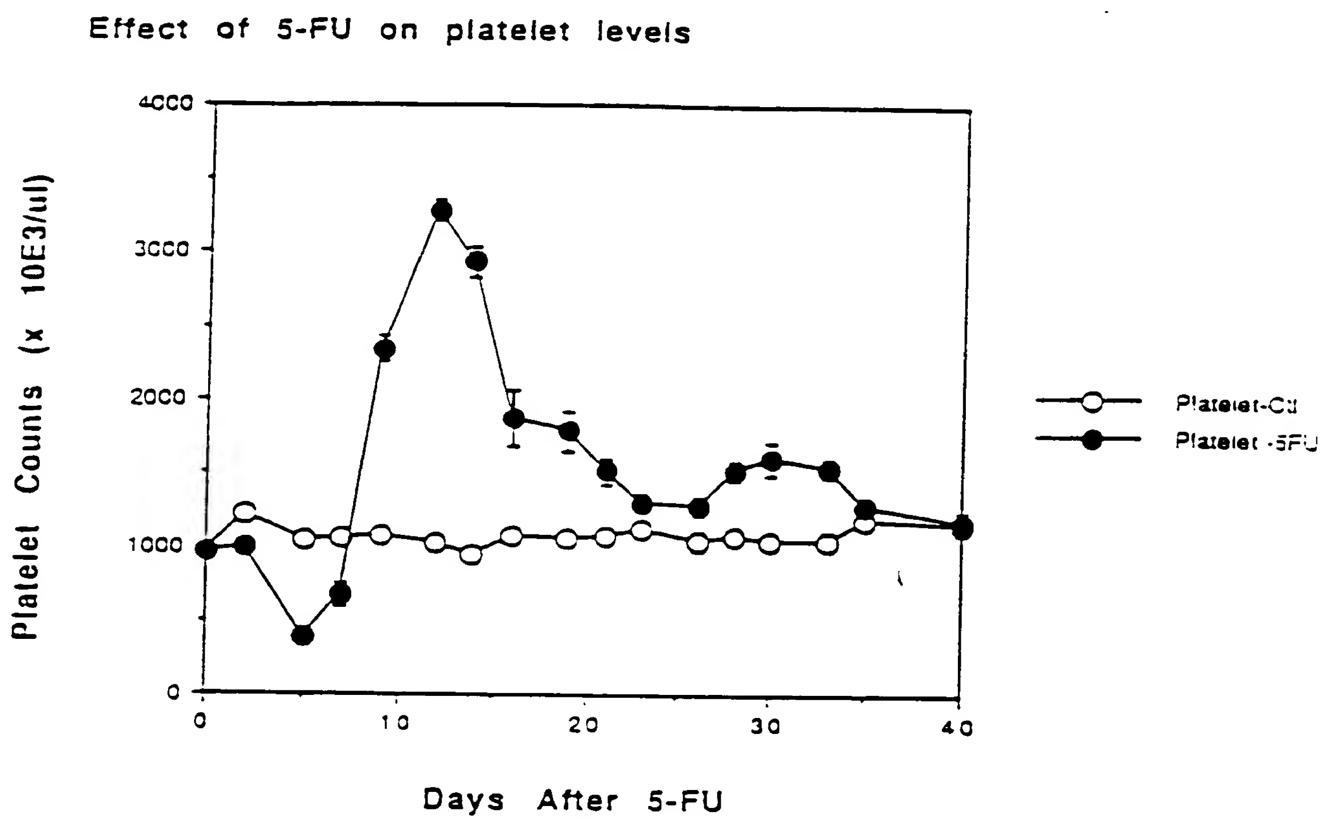
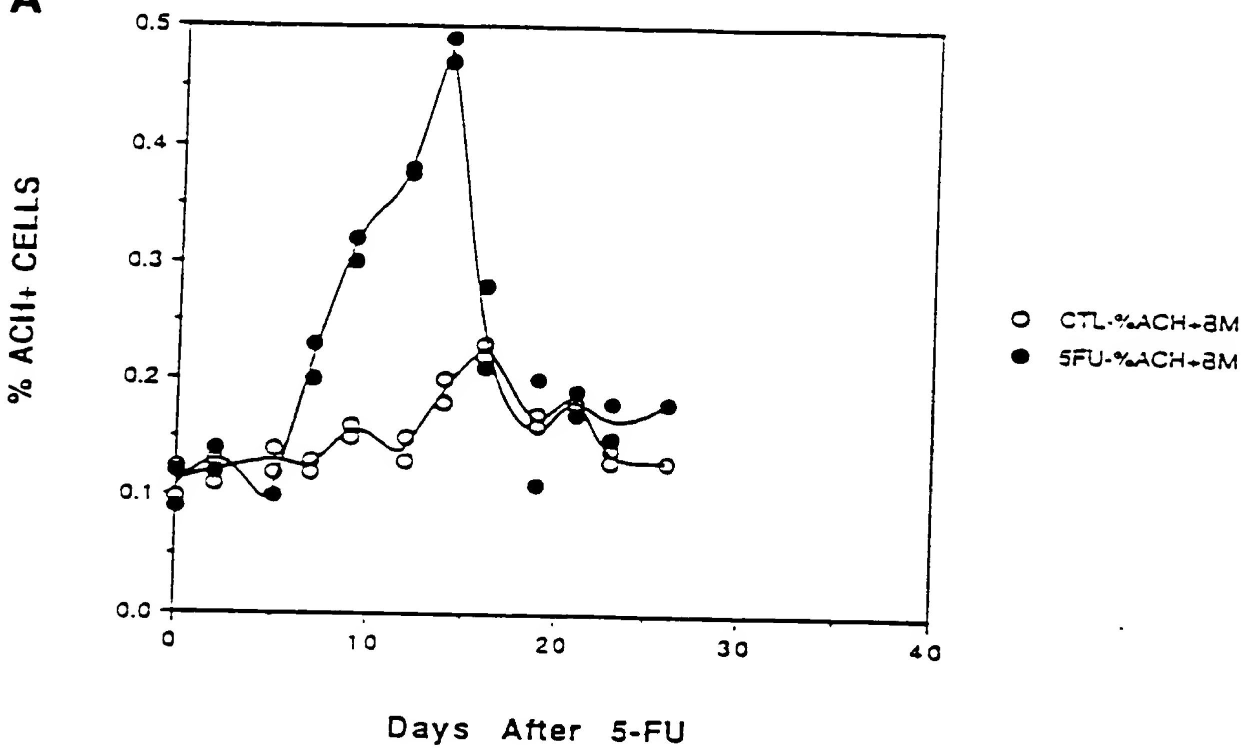

Effect of 5-FU on platelet levels
Platelet Counts (x 10E3/ul)
4000
3000
2000
1000
0
0
10
20
30
40
Days After 5-FU
Platelet-Ctl
Platelet -5FU

FIG. 56

5-FU Effect on ACH+ Cells in Marrow

A



5-FU Effect on ACH+ Cells in Spleen

B

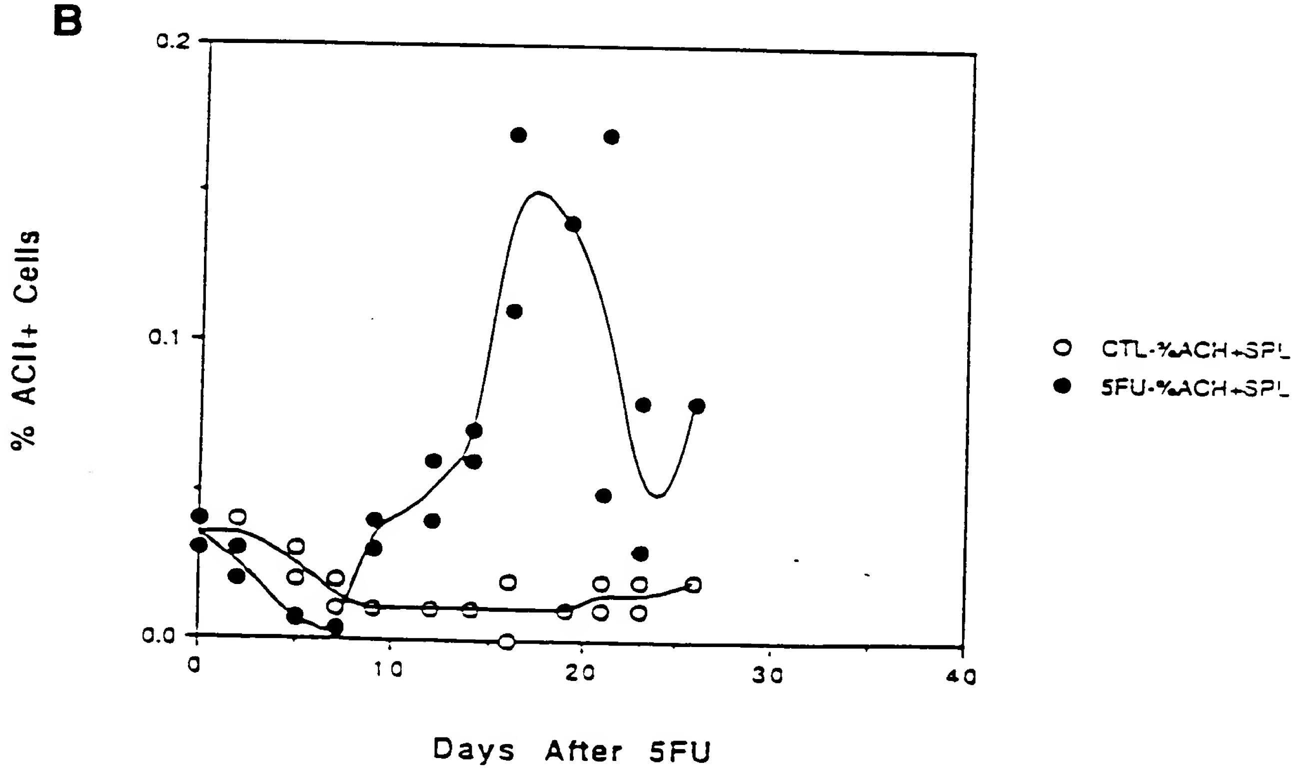
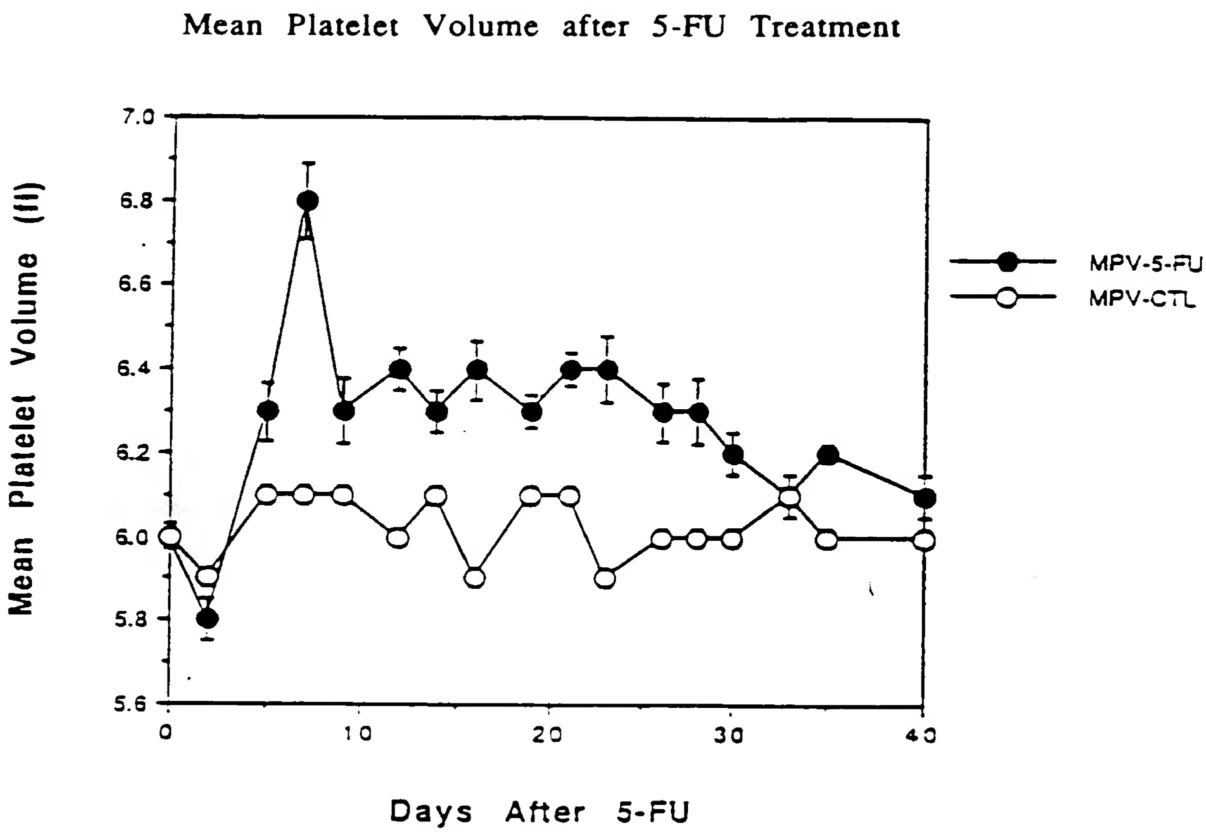
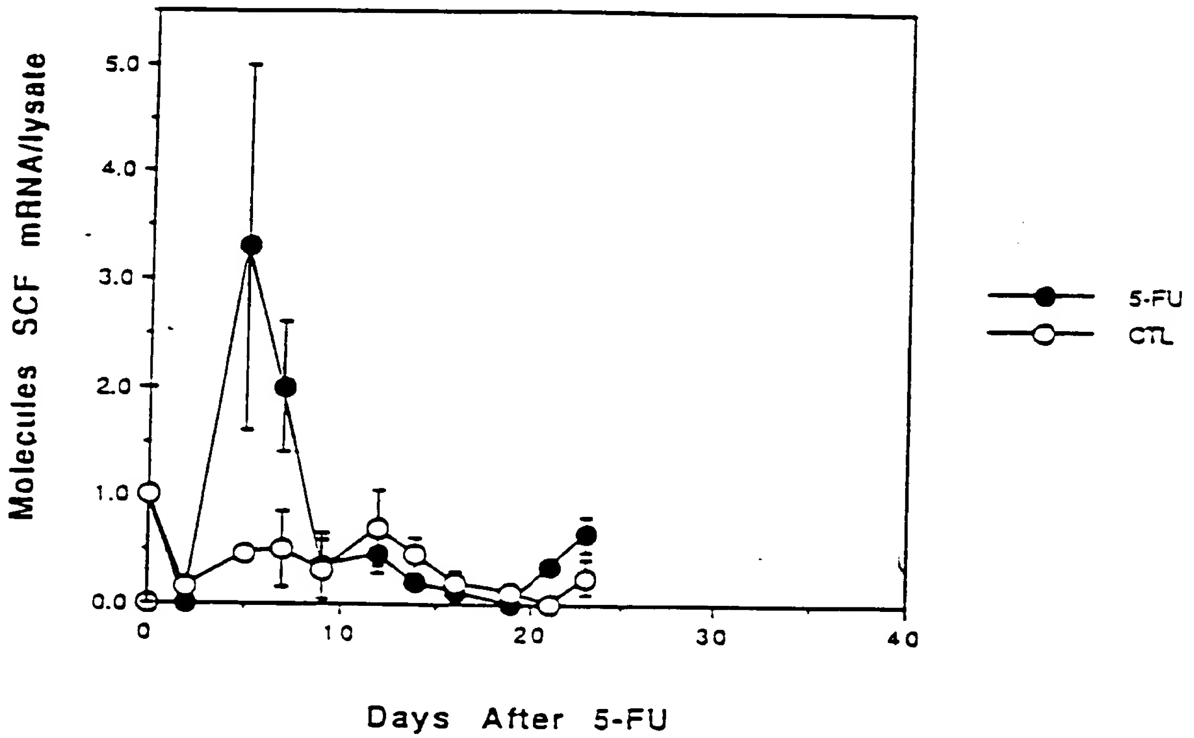


FIG. 57



Mean Platelet Volume after 5-FU Treatment
Mean Platelet Volume (fl)
7.0
6.8
6.6
6.4
6.2
6.0
5.8
5.6
0
10
20
30
40
Days After 5-FU
MPV-5-FU
MPV-CTL

FIG. 58



Molecules SCF mRNA/lysate
5.0
4.0
3.0
2.0
1.0
0.0
0
10
20
30
40
Days After 5-FU
5-FU
CTL

FIG. 59

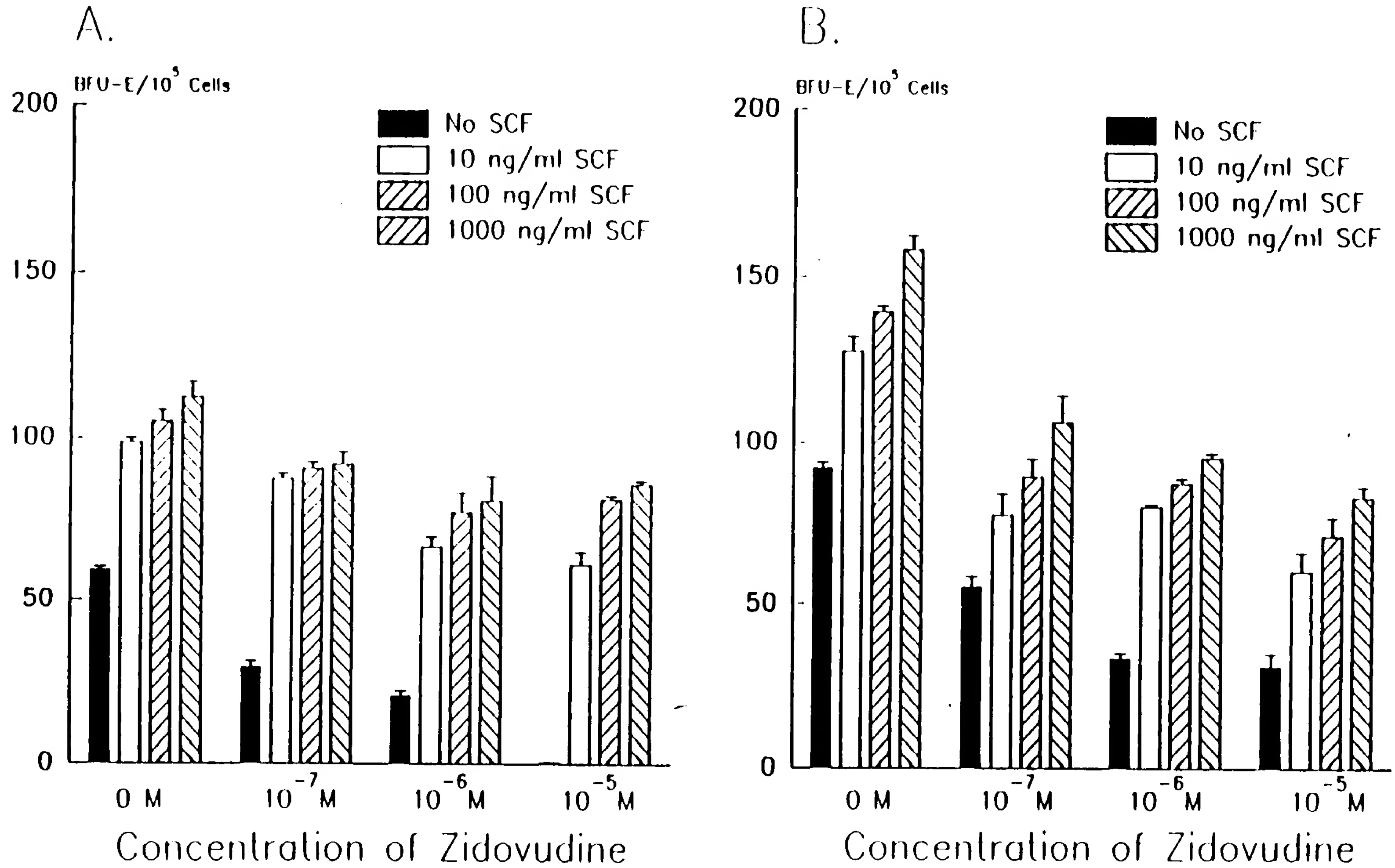
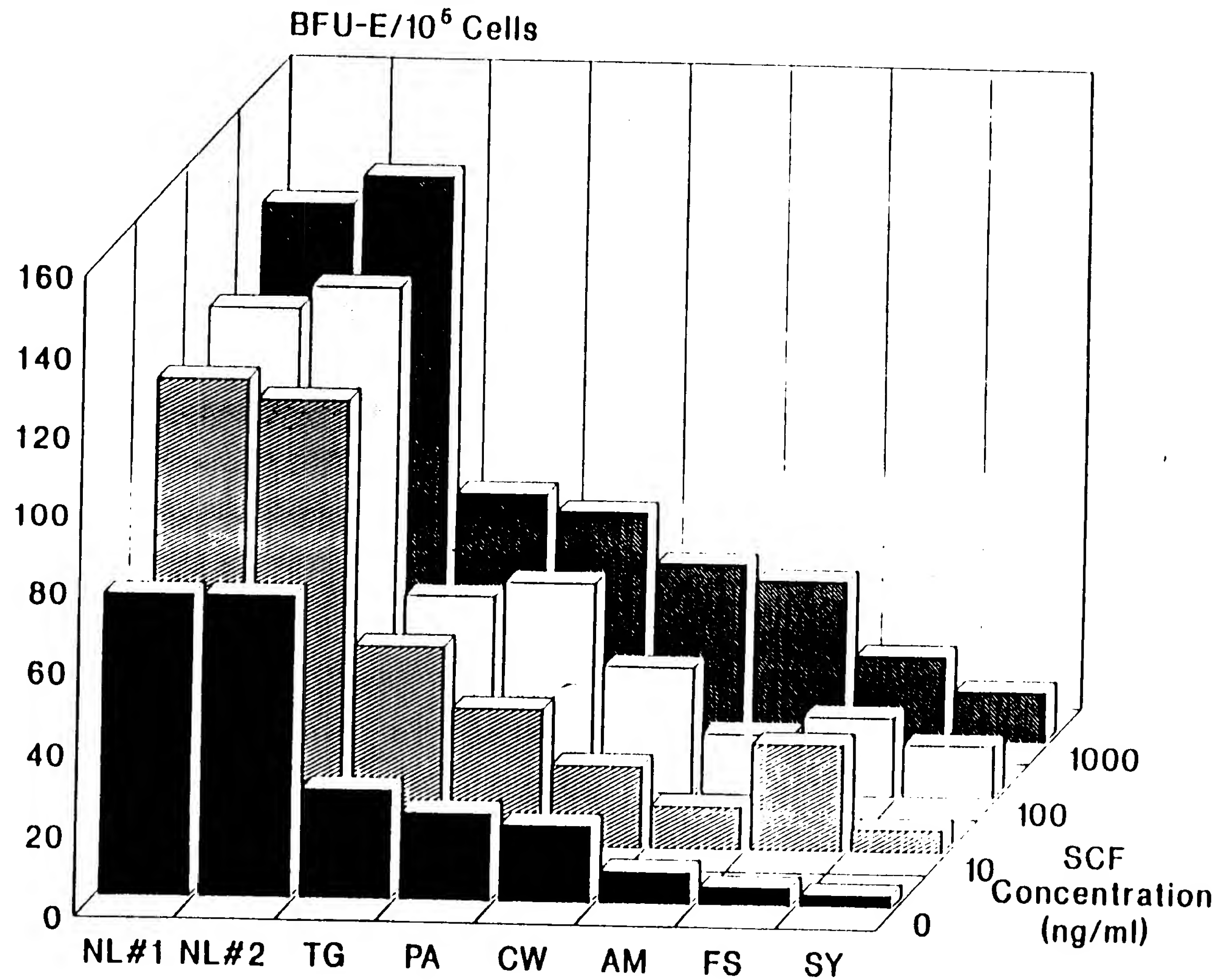
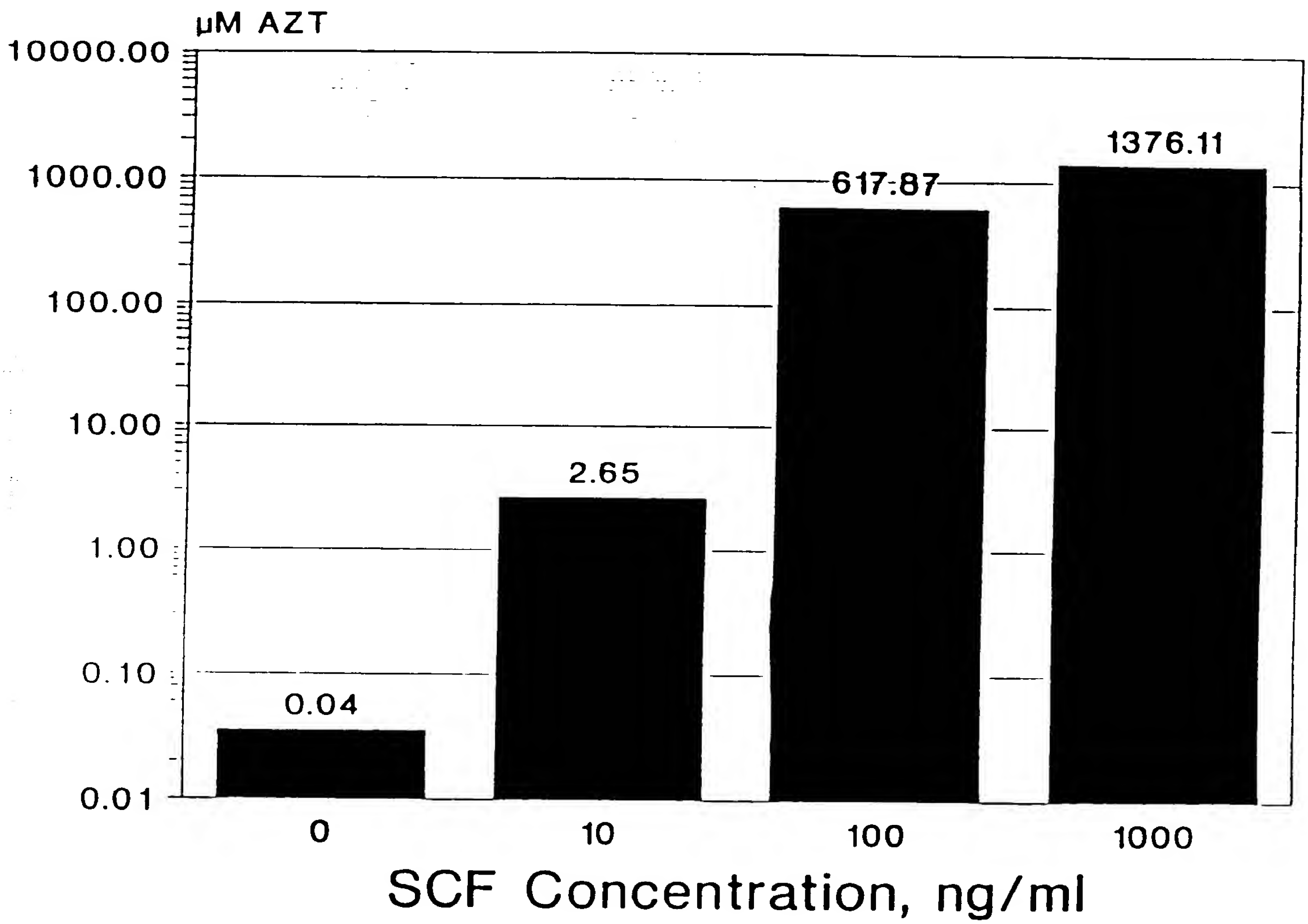

A.
BFU-E/10^5 Cells
200
150
100
50
0
No SCF
10 ng/ml SCF
100 ng/ml SCF
1000 ng/ml SCF
0 M
10^{-7} M
10^{-6} M
10^{-5} M
Concentration of Zidovudine
B.
BFU-E/10^5 Cells
200
150
100
50
0
No SCF
10 ng/ml SCF
100 ng/ml SCF
1000 ng/ml SCF
0 M
10^{-7} M
10^{-6} M
10^{-5} M
Concentration of Zidovudine

FIG. 60



BFU-E/10^5 Cells
160
140
120
100
80
60
40
20
0
NL#1
NL#2
TG
PA
CW
AM
FS
SY
1000
100
10
0
SCF
Concentration
(ng/ml)

FIG. 61



μM AZT
10000.00
1000.00
100.00
10.00
1.00
0.10
0.01
0.04
2.65
617.87
1376.11
0
10
100
1000
SCF Concentration, ng/ml

FIG. 62

EFFECT OF SCF ON AZT SUPPRESSION OF BMC

BFU-E

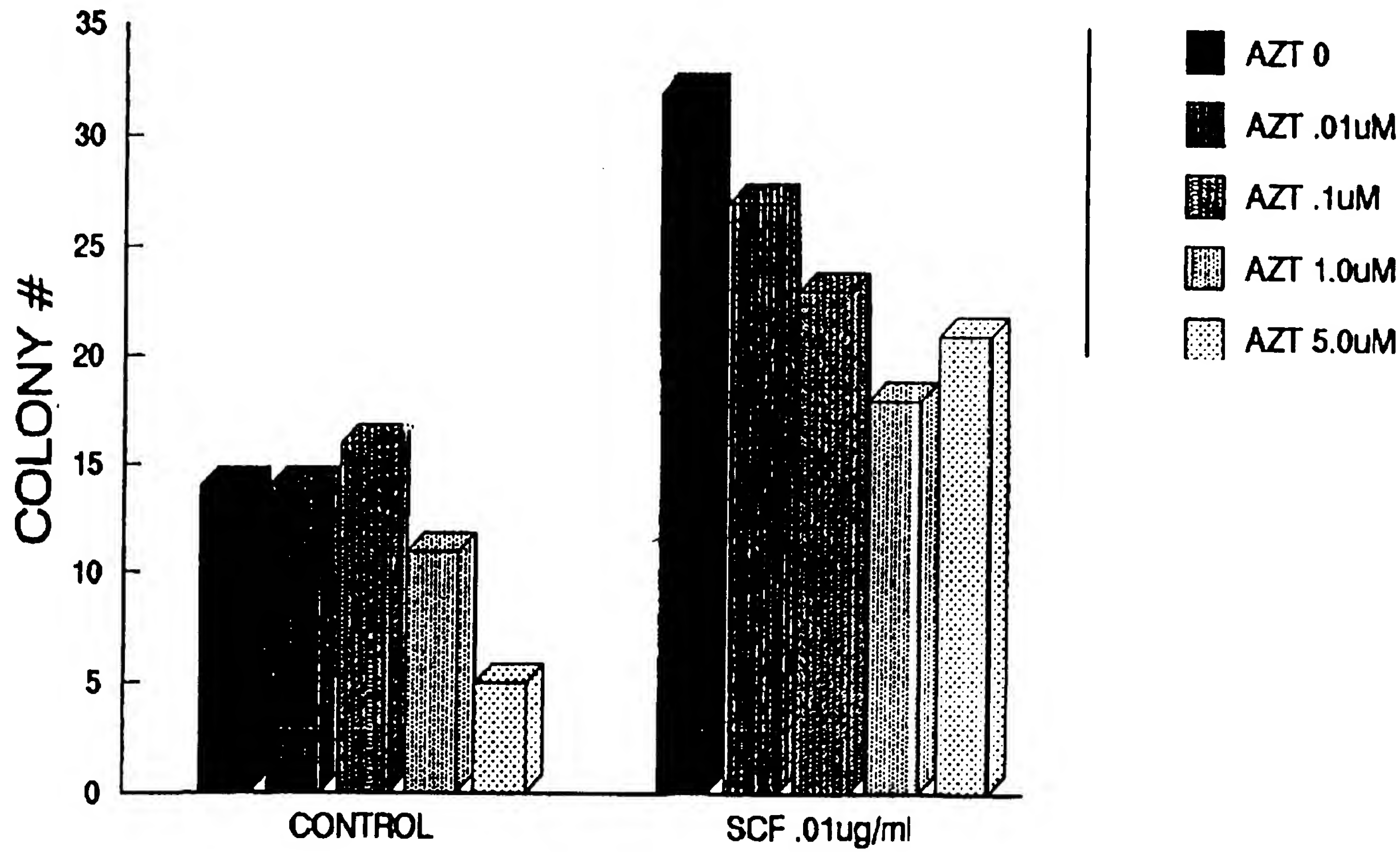


FIG. 63

EFFECT OF SCF ON AZT SUPPRESSION OF BMC

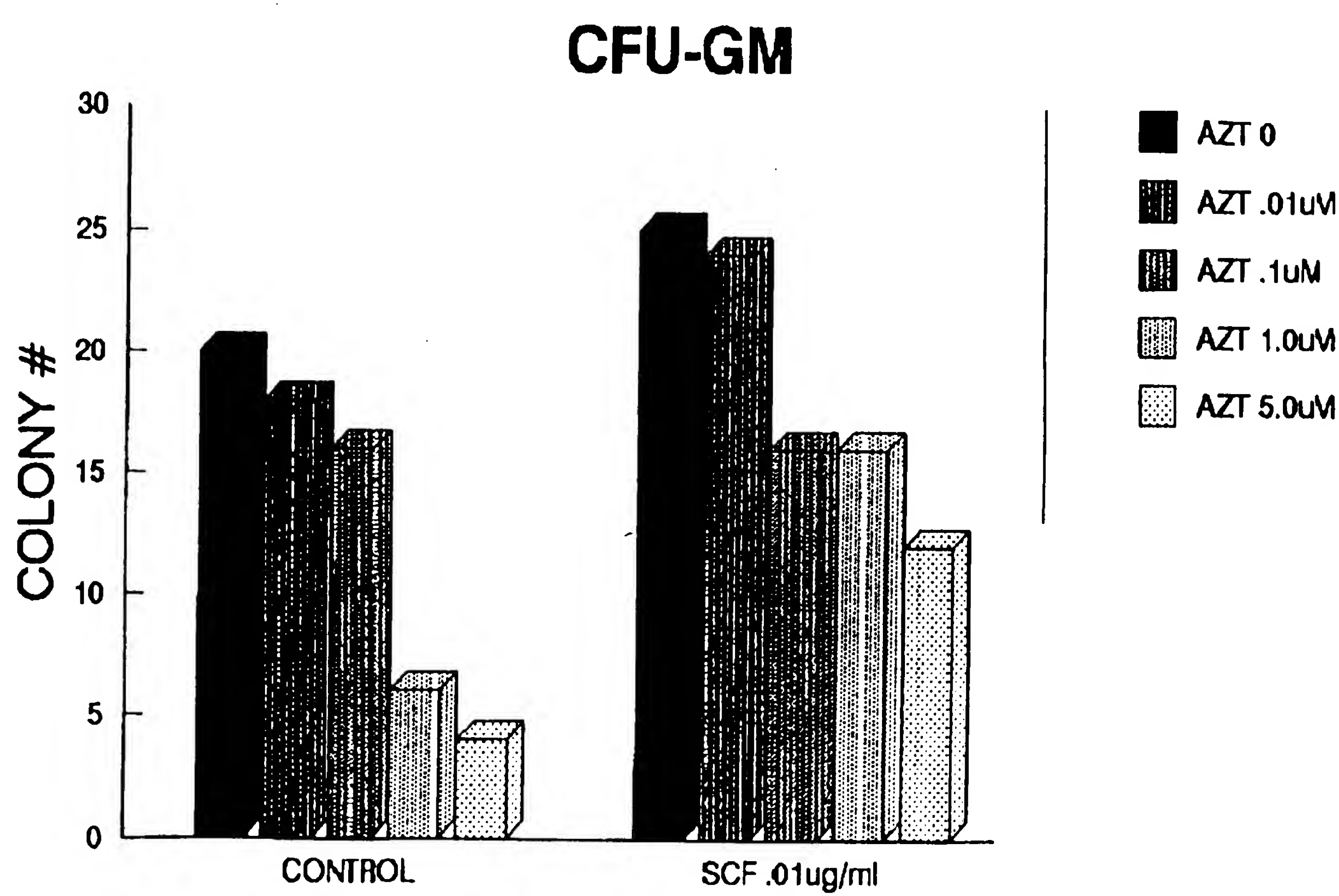


FIG. 64

EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC

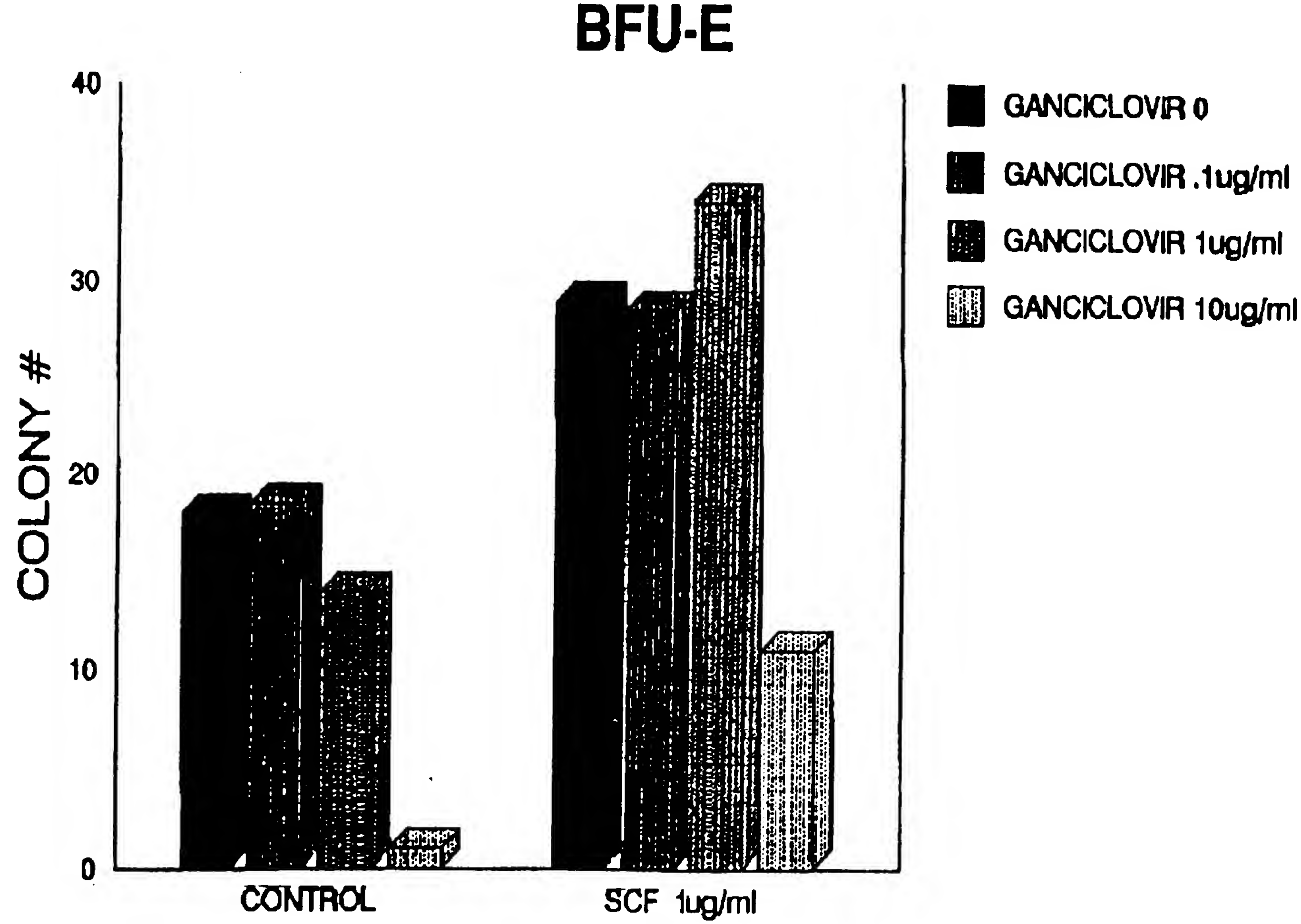


FIG. 65

EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC

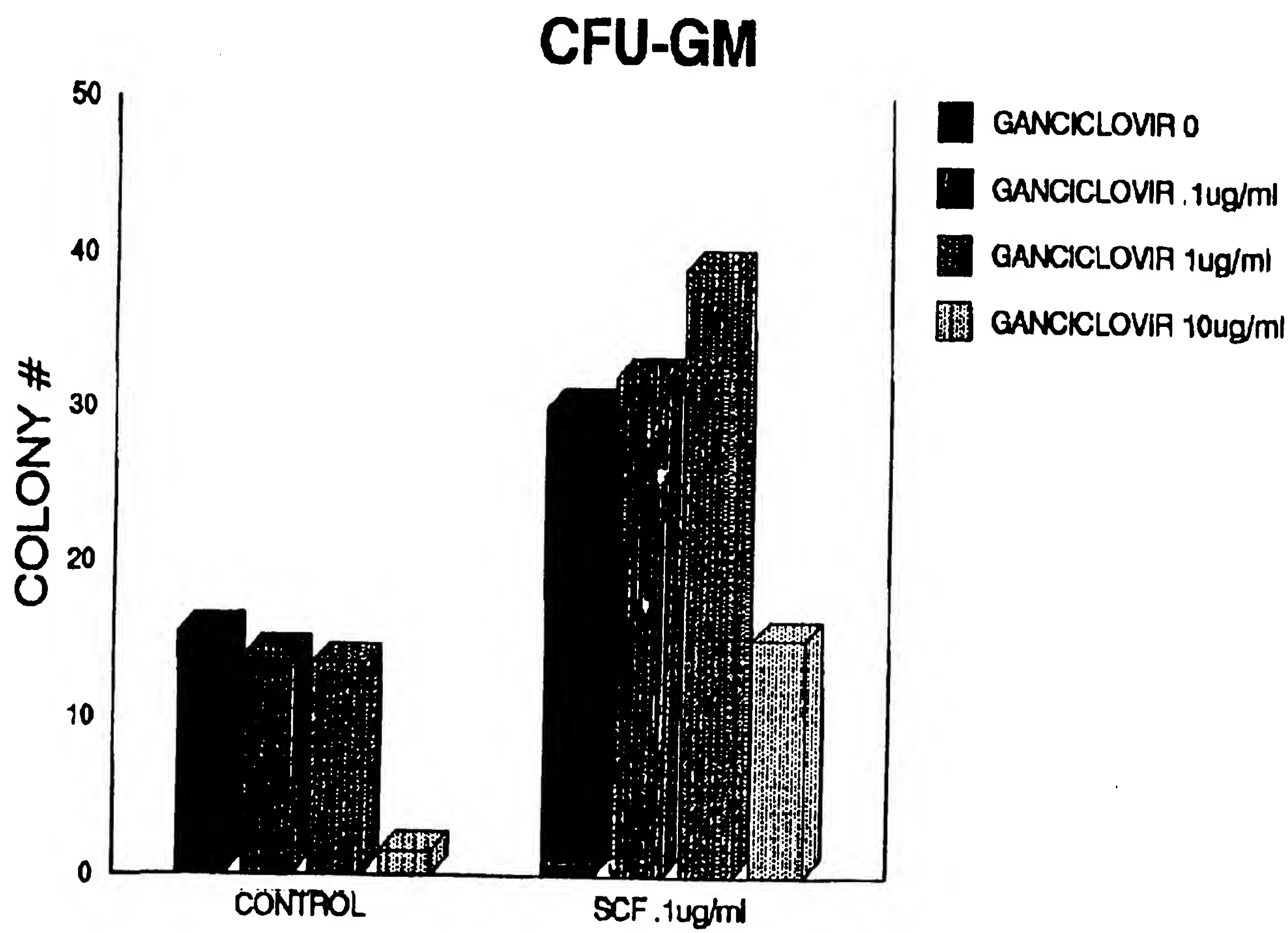


FIG. 66

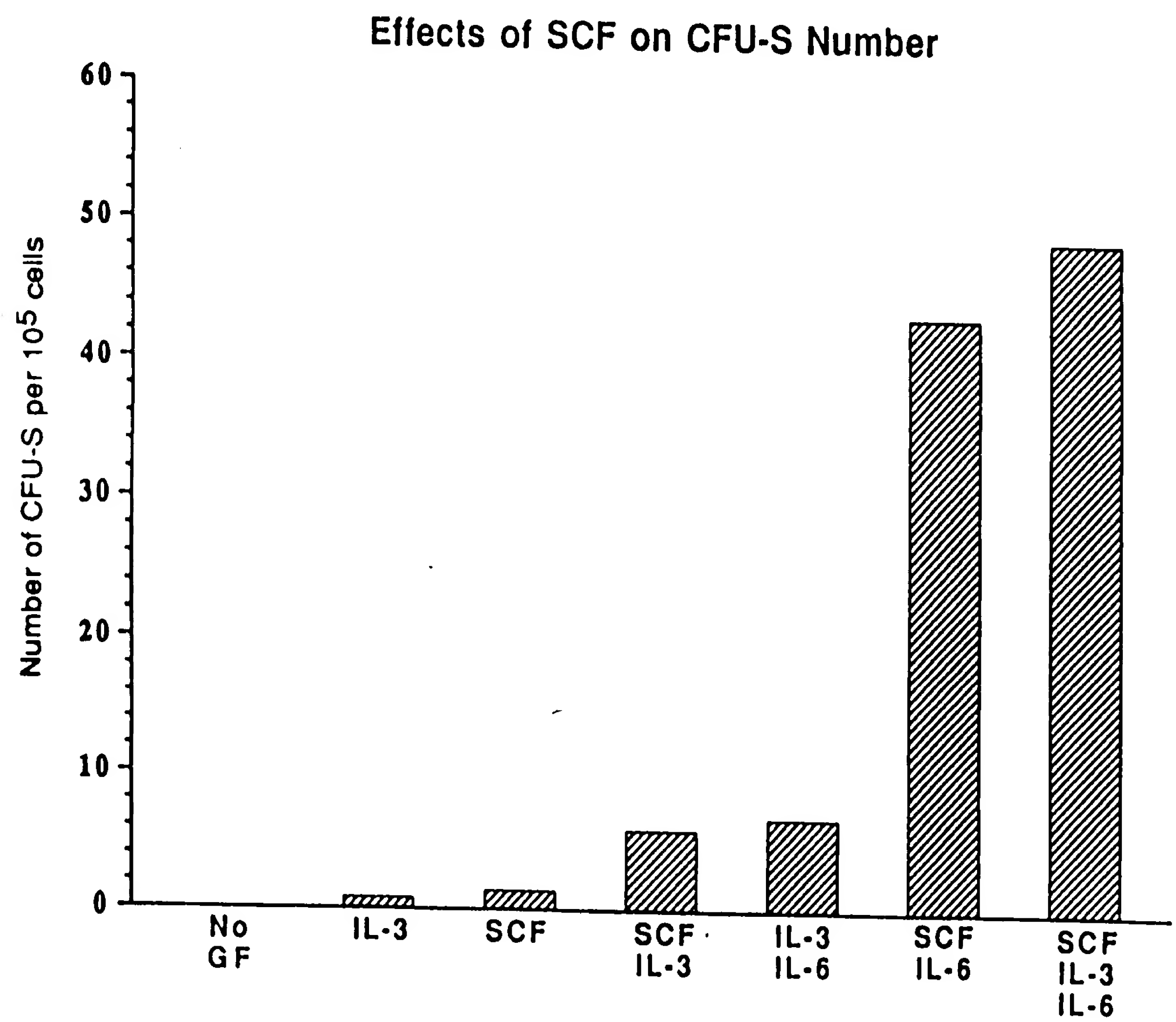
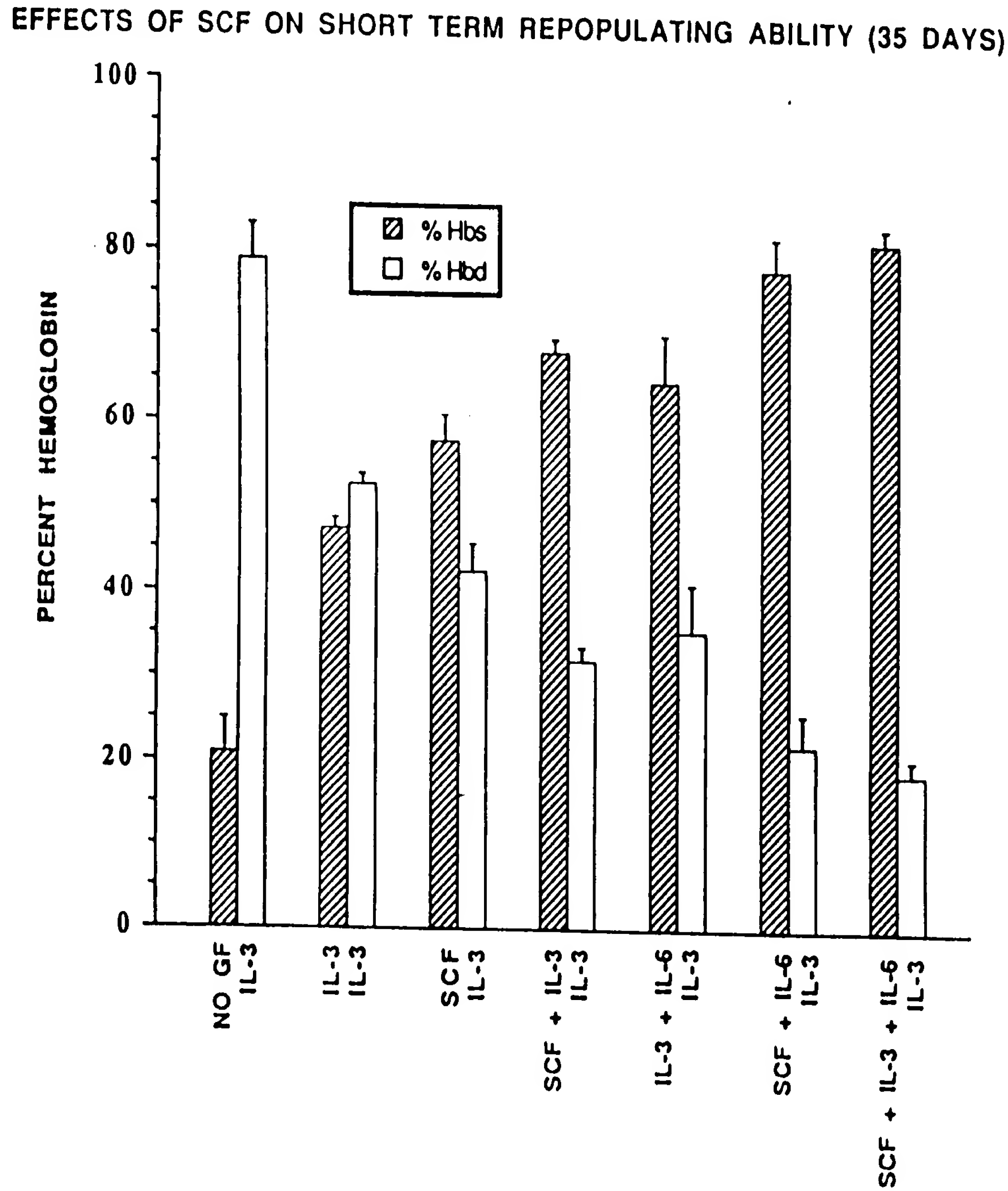

Effects of SCF on CFU-S Number
Number of CFU-S per 10^5 cells
0
10
20
30
40
50
60
No GF
IL-3
SCF
SCF IL-3
IL-3 IL-6
SCF IL-6
SCF IL-3 IL-6

FIG. 67



EFFECTS OF SCF ON SHORT TERM REPOPULATING ABILITY (35 DAYS)
PERCENT HEMOGLOBIN
100
80
60
40
20
0
% Hbs
% Hbd
NO GF IL-3
IL-3 IL-3
SCF IL-3
SCF + IL-3 IL-3
IL-3 + IL-6 IL-3
SCF + IL-6 IL-3
SCF + IL-3 + IL-6 IL-3

FIG. 68

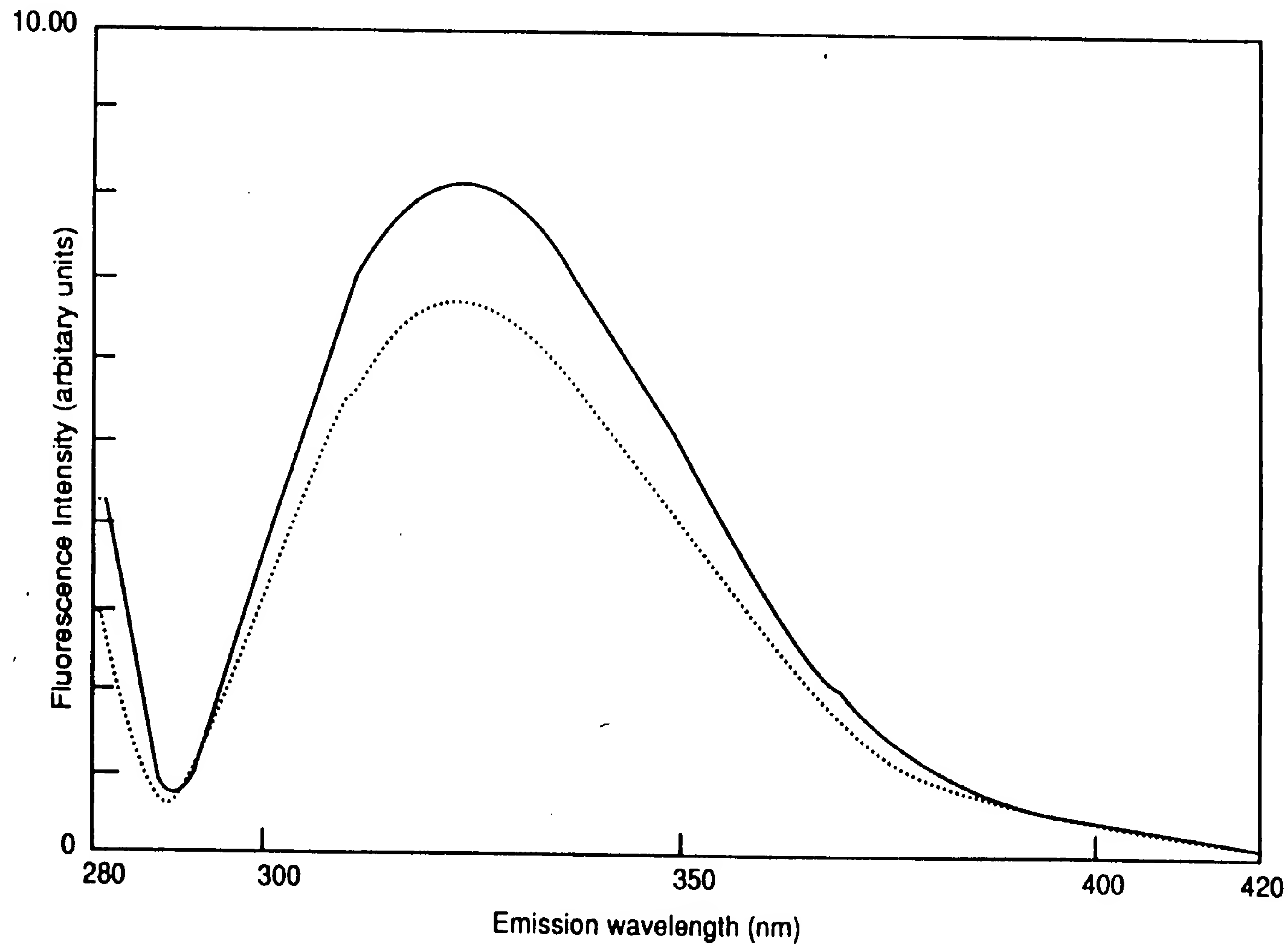

10.00
0
Fluorescence Intensity (arbitary units)
280
300
350
400
420
Emission wavelength (nm)

FIG. 69A

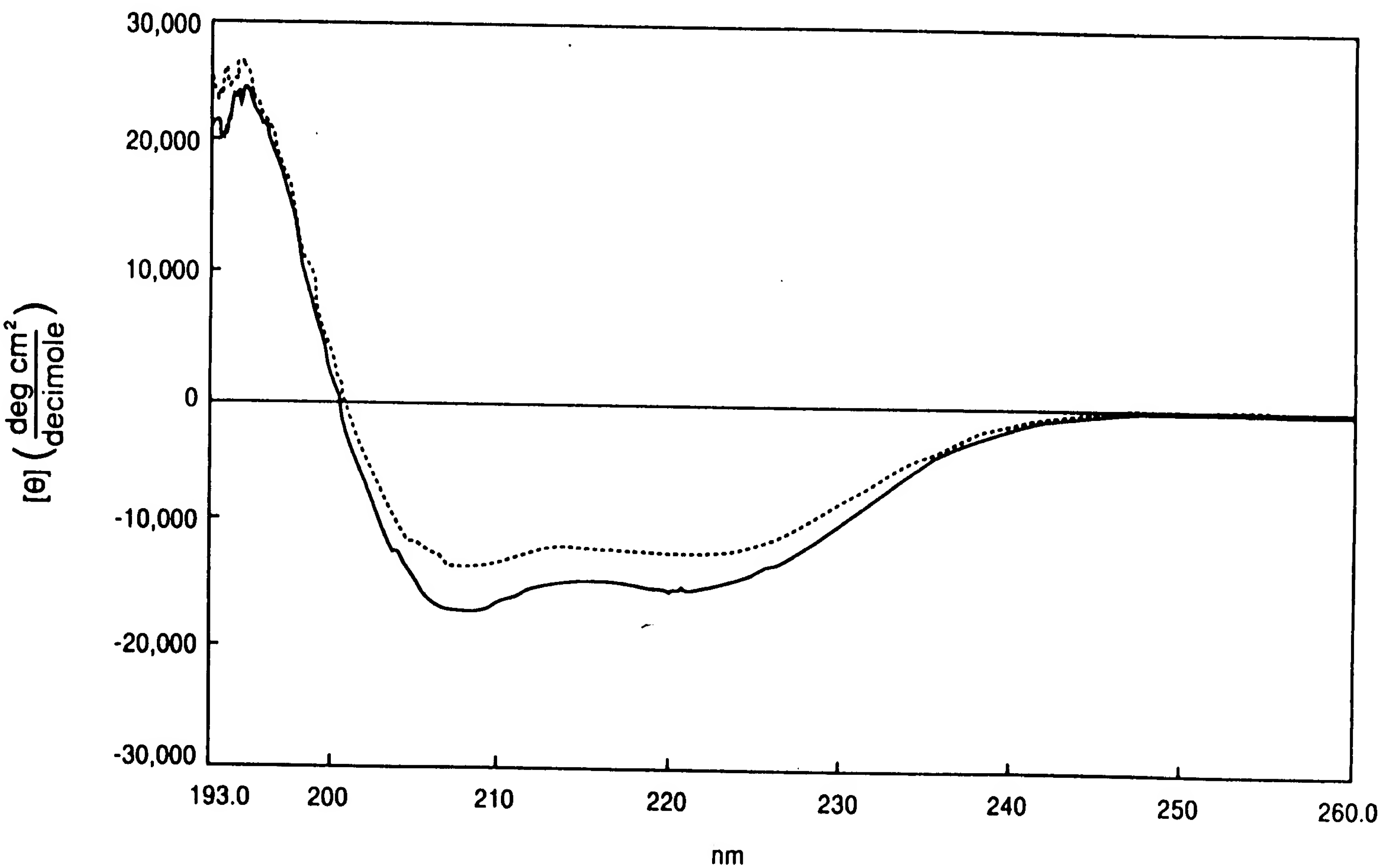
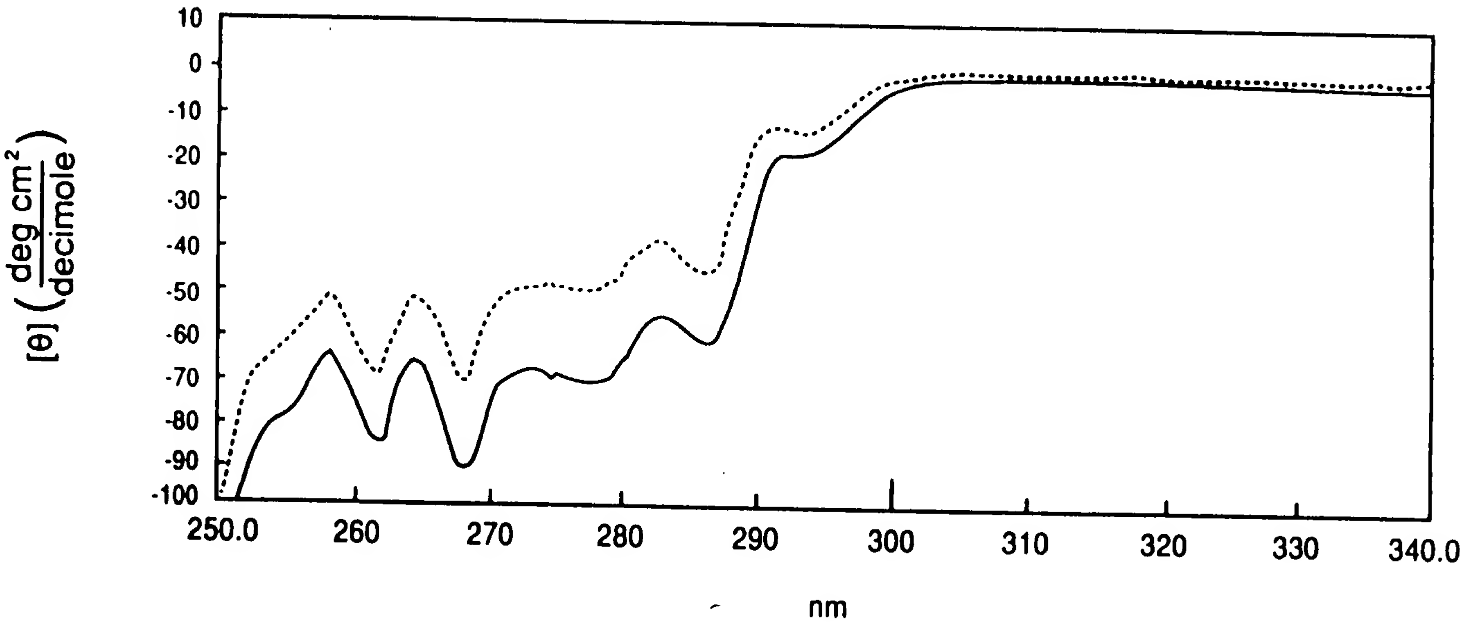

30,000
20,000
10,000
0
-10,000
-20,000
-30,000
[θ] (deg cm² / decimole)
193.0
200
210
220
230
240
250
260.0
nm

FIG. 69B



[θ] (deg cm²/decimole)
10
0
-10
-20
-30
-40
-50
-60
-70
-80
-90
-100
250.0
260
270
280
290
300
310
320
330
340.0
nm

FIG. 70